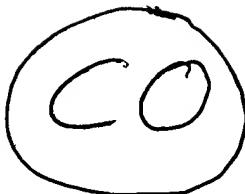


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(54) Title: METHOD OF TREATING DOPAMINERGIC AND GABA-NERGIC DISORDERS					
(57) Abstract					
It is shown here that <i>hedgehog</i> proteins or mimicking agents possess novel activities beyond phenotype specification. Using cultures derived from the embryonic day 14.5 (E14.5) rat ventral mesencephalon, we show that <i>hedgehog</i> or mimicking agents are also trophic for dopaminergic neurons. Interestingly, <i>hedgehog</i> or mimicking agents not only promote dopaminergic neuron survival, but also promote the survival of midbrain GABA-immunoreactive (GABA-ir) neurons.					

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METHOD OF TREATING DOPAMINERGIC AND GABA-NERGIC DISORDERS

BACKGROUND OF THE INVENTION

5 The individual symptoms of Parkinson's disease have been described by physicians from the time of Galen, but their occurrence as a syndrome was not recognized until 1817. In that year James Parkinson, a London physician, published an essay in which he argued that several different motor symptoms could be considered together as a group forming a distinctive condition. His observations are interesting not
10 only because his conclusion was correct but also because he made his observations in part at a distance by watching the movements of Parkinsonian victims in the street of London. Parkinson's disease has been called at different times the shaking palsy or its Latin equivalent, paralysis agitans, but received its commoner designation from Jean Charcot, who suggested that the disease be renamed to honor James Parkinson's
15 recognition of its essential nature.

20 Parkinson's disease is fairly common, estimates of its incidence varying from 0.1 to 1.0% of the population. It is also of considerable interest for a number of other reasons. First, the disease seems related to the degeneration of the substantia nigra, and to the loss of the neurotransmitter substance dopamine, which is produced by cells of this nucleus. The disease, therefore, provides an important insight into the role of this brainstem nucleus and its neurotransmitter in the control of movement. Second, because a variety of pharmacological treatments for Parkinson's disease relieve different features of its symptoms to some extent the disease provides a model for understanding pharmacological treatments of motor disorders in their more general
25 aspects. Third, although Parkinson's disease is described as a disease entity, the symptoms vary enormously among people, thus making manifest the complexity with which the components of movement are organized to produce fluid motion. Fourth, because many of the symptoms of Parkinson's disease strikingly resemble changes in motor activity that occur as a consequence of aging, the disease provides indirect
30 insight into the more general problems of neural changes in aging.

There are three major types of Parkinson's disease: idiopathic, postencephalitic, and drug-induced. Parkinson's diseases may also result from arteriosclerosis, may follow poisoning by carbon monoxide or manganese intoxication, or may result from syphilis or the development of tumors. As is suggested by its name, the idiopathic

cause of Parkinson's disease is not known. Its origin may be familiar, or it may be part of the aging process, but it is also widely thought that it might have a viral origin. It most often occurs in people who are over 50 years of age. The postencephalitic form originated in the sleeping sickness that appeared in the winter of 1916-1917 and 5 vanished by 1927. Although the array of symptoms was bewilderingly varied; such that hardly any two patients seemed alike, Constantin von Economo demonstrated a unique pattern of brain damage associated with a virus infection in the brains of patients who had died from the disease. A third of those affected died in the acute stages of sleeping sickness in states either of coma or of sleeplessness. Although many people seemed to 10 completely recover from the sickness, most subsequently developed neurological or psychiatric disorders and parkinsonism. The latency between the initial and subsequent occurrences of the disease has never been adequately explained. Specified searches for viral particles or virus specific products in Parkinson patients have revealed no evidence of viral cause. The third major cause of Parkinson's disease is more recent, 15 and is associated with ingestion of various drugs, particularly major tranquilizers that include reserpine and several phenothiazine and butyrophenone derivatives. The symptoms are usually reversible, but they are difficult to distinguish from those of the genuine disorder.

Recently it has been found that external agents can cause symptoms quite 20 rapidly. Langston and coworkers have reported that a contaminant of synthetic heroin, MPTP, when taken by drug users, is converted into MPP which is extremely toxic to dopamine cells. A number of young drug users were found to display a complete parkinsonian syndrome after using contaminated drugs. This finding has suggested that other substances might cause similar effects. Demographic studies of patient admission 25 in the cities of Vancouver and Helsinki show an increase in the incidence of patients getting the disease at ages younger than 40. This has raised the suggestion that water and air might contain environmental toxins that work in a fashion similar to MPTP.

Although Parkinsonian patients can be separated into clinical groups on the basis of cause of the disease, it is nevertheless likely that the mechanisms producing the 30 symptoms have a common origin. Either the substantia nigra is damaged, as occurs in idiopathic and postencephalitic cases, or the activity of its cells is blocked, or cells are killed, as occurs in drug induced parkinsonism. The cells of the substantia nigra contain a dark pigment in Parkinson's disease this area is depigmented by degeneration of the melatonin containing neurons of the area. The cells of the substantia nigra are the point 35 of origin of fibers that go to the basal ganglia frontal cortex and to the spinal cord. The neurotransmitter at the synapses of these projection is dopamine. It has been

demonstrated by bioassay of the brains of deceased parkinsonian patients, and by analysis of the major metabolite of dopamine, homovanillic acid, which is excreted in the urine, that the amount of brain dopamine is reduced by over 90% and is often reduced to undetectable amounts. Thus the cause of Parkinson's disease has been 5 identified with some certainty as a lack of dopamine or in drug induced cases with a lack of dopamine action.

Certain attempts have been made to treat Parkinson's disease. One proposed treatment for Parkinson's disease is Sinemet CR, which is a sustained-release tablet containing a mixture of carbidopa and levodopa, available from The DuPont Merck 10 Pharmaceutical Co. Another proposed treatment for Parkinson's disease is Eldepryl, which is a tablet containing selegiline hydrochloride, available from Somerset Pharmaceuticals, Inc. Another proposed treatment for Parkinson's disease is Parlodel, which is a tablet containing bromocriptine mesylate, available from Sandoz Pharmaceuticals Corporation.

15

SUMMARY OF THE INVENTION

One aspect of the present application relates to a method for promoting the survival of dopaminergic or GABAergic neurons by contacting the cells, *in vitro* or *in vivo*, with a hedgehog therapeutic or ptc therapeutic in an amount effective increasing 20 the rate of survival of the neurons relative to the absence of administration of the hedgehog therapeutic or ptc therapeutic.

One aspect of the present application relates to a method for promoting the survival of neurons of the substantia nigra by contacting the cells, *in vitro* or *in vivo*, with a hedgehog therapeutic or ptc therapeutic in an amount effective increasing the 25 rate of survival of the neurons relative to the absence of administration of the hedgehog therapeutic or ptc therapeutic.

In other embodiments, the subject method can be used for protecting dopaminergic and/or GABAergic neurons of a mammal from neurodegeneration; for preventing or treating neurodegenerative disorder; for treatment of Parkinson's; for 30 treatment of Huntington's; and/or for treatment of ALS. In embodiments wherein the patient is treated with a ptc therapeutic, such therapeutics are preferably small organic molecules which mimic *hedgehog* effects on *patched*-mediated signals.

Wherein the subject method is carried out using a *hedgehog* therapeutic, the *hedgehog* therapeutic, preferably a polypeptide including a *hedgehog* portion

comprising at least a bioactive extracellular portion of a *hedgehog* protein, e.g., the *hedgehog* portion includes at least 50, 100 or 150 amino acid residues of an N-terminal half of a *hedgehog* protein. In preferred embodiments, the *hedgehog* portion includes at least a portion of the *hedgehog* protein corresponding to a 19kd fragment of the 5 extracellular domain of a *hedgehog* protein.

In preferred embodiments, the *hedgehog* portion has an amino acid sequence at least 60, 75, 85, or 95 percent identical with a *hedgehog* protein of any of SEQ ID Nos. 10-18 or 20, though sequences identical to those sequence listing entries are also contemplated as useful in the present method. The *hedgehog* portion can be encoded 10 by a nucleic acid which hybridizes under stringent conditions to a nucleic acid sequence of any of SEQ ID Nos. 1-9 or 19, e.g., the *hedgehog* portion can be encoded by a vertebrate *hedgehog* gene, especially a human *hedgehog* gene.

In other embodiments, the subject method can be carried out by administering a 15 gene activation construct, wherein the gene activation construct is designed to recombine with a genomic *hedgehog* gene of the patient to provide a heterologous transcriptional regulatory sequence operatively linked to a coding sequence of the *hedgehog* gene.

In still other embodiments, the subject method can be practiced with the 20 administration of a gene therapy construct encoding a *hedgehog* polypeptide. For instance, the gene therapy construct can be provided in a composition selected from a group consisting of a recombinant viral particle, a liposome, and a poly-cationic nucleic acid binding agent.

Another aspect of the present invention relates to the cloning of various human 25 *hedgehog* genes, e.g., human *Dhh* and *Ihh*. In a preferred embodiment, there is provided an isolated and/or recombinantly produced polypeptide comprising an amino acid sequence which is at least 95 percent identical to a sequence represented by SEQ ID. NO. 16 or 17, or a bioactive extracellular fragment thereof. In another embodiment, there is provided an isolated and/or recombinantly produced polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to a sequence 30 selected from the group consisting of SEQ ID. NO. 16 and SEQ ID. NO. 17. In a preferred embodiment, the polypeptide is formulated in a pharmaceutically acceptable carrier.

Preferred bioactive fragments of the human *Ihh* and *Dhh* proteins include from 35 about residues 28-202 of SEQ ID No. 16 and 23-198 of SEQ ID No. 17, respectively. Longer or shorter fragments are contemplated, as for example, those which are 5, 10, 15

or 20 amino acids shorter on either or both the N-terminal and C-terminal ends of the fragment.

In certain embodiments, the polypeptide is purified to at least 80% by dry weight, and more preferably 90 or 95% by dry weight.

5 Another aspect of the present invention provides an isolated nucleic acid encoding a polypeptide comprising a *hedgehog* amino acid sequence which is at least 95 percent identical to a *hedgehog* protein selected from the group consisting of SEQ ID No:16 and SEQ ID No:17, or bioactive fragments thereof, e.g., the *hedgehog* amino acid sequence (i) binds to a *patched* protein, (ii) regulates differentiation of neuronal 10 cells, (iii) regulates survival of differentiated neuronal cells, (iv) regulates proliferation of chondrocytes, (v) regulates proliferation of testicular germ line cells, or (vi) functionally replaces *drosophila hedgehog* in transgenic *drosophila* fly, or a combination thereof.

15 In other preferred embodiments, the isolated nucleic acid encodes a polypeptide having a *hedgehog* amino acid sequence encoded by a nucleic acid which hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID No:7 and SEQ ID No:8, which *hedgehog* amino acid sequence of the polypeptide corresponds to a natural proteolytic product of a *hedgehog* protein. Such polypeptides preferably (i) bind to a *patched* protein, (ii) regulate differentiation of 20 neuronal cells, (iii) regulate survival of differentiated neuronal cells, (iv) regulate proliferation of chondrocytes, (v) regulate proliferation of testicular germ line cells, and/or (vi) functionally replace *drosophila hedgehog* in transgenic *drosophila* fly, or a combination thereof.

25 In preferred embodiments, the nucleic acid encodes a *hedgehog* amino acid sequence identical to a *hedgehog* protein selected from the group consisting of SEQ ID No:16 and SEQ ID No:17.

Another preferred embodiment provides an isolated nucleic acid comprising a coding sequence of a human *hedgehog* gene, encoding a bioactive *hedgehog* protein.

30 Still another aspect of the present invention relates to an expression vector, capable of replicating in at least one of a prokaryotic cell and eukaryotic cell, comprising a nucleic acid encoding a *Dhh* or *Ihh* polypeptide described above.

The present invention also provides a host cell transfected with such expression vectors; as well as methods for producing a recombinant *hedgehog* polypeptide by

culturing such cells in a cell culture medium to express a *hedgehog* polypeptide and isolating said *hedgehog* polypeptide from the cell culture.

Still another aspect of the present invention provides a recombinant transfection system, e.g., such as may be useful for gene therapy, comprising (i) a gene construct including the coding sequence for a human *Ihh* or *Dhh* protein, operably linked to a transcriptional regulatory sequence for causing expression of the *hedgehog* polypeptide in eukaryotic cells, and (ii) a gene delivery composition for delivering said gene construct to a cell and causing the cell to be transfected with said gene construct. For instance, the gene delivery composition is selected from a group consisting of a recombinant viral particle, a liposome, and a poly-cationic nucleic acid binding agent.

Another aspect of the present invention provides a probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of SEQ ID No. 7 or 8, or naturally occurring mutants thereof. In preferred embodiments, the probe/primer includes a label group attached thereto and able to be detected. The present invention also provides a test kit for detecting cells which contain a *hedgehog* mRNA transcript, and includes such probe/primers.

Still another embodiment of the present invention provides a purified preparation of an antisense nucleic acid which specifically hybridizes to and inhibits expression of a gene encoding a human *Ihh* or *Dhh* *hedgehog* protein under physiological conditions, which nucleic acid is at least one of (i) a synthetic oligonucleotide, (ii) single-stranded, (iii) linear, (iv) 20 to 50 nucleotides in length, and (v) a DNA analog resistant to nuclease degradation.

25

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. *Shh* and *Ptc* in the E14.5 rat embryo. *Shh* (A, antisense; B, sense control), and *ptc* (C, antisense; D, sense control) expression as detected by *in situ* hybridization with digoxigenin-labeled riboprobes and alkaline phosphataseconjugated 30 anti-digoxigenin. The arrow in A and the double-arrow in C designate the zona limitan intrathalamica. Major anatomical structures and summary diagrams of *shh* and *ptc* expression are shown in E. Scale bar = 1 mm.

Figure 2. *Shh* promotes the survival of TH+ neurons of the ventral mesencephalon. (A) Timecourse and dose response of the *Shh* effect. The number of

TH⁺ neurons in control cultures (0 ng/ml Shh) began to decline dramatically by 5 days *in vitro*. In cultures treated with Shh at 25 and 50 ng/ml there were significantly greater numbers of TH⁺ neurons over control- through 24 days *in vitro* (from 5 to 24 days, p <.001 at 25 and 50 ng/ml). The 50 ng/ml dose typically gave a 50-100% increase over 5 controls at all time points (error bars s.e.m.) Photomicrographs of TH⁺ neurons in 50 ng/ml Shh treated (B,D) and control (C, E) cultures, 2 days (B, C) and 7 days (D, E) post-plating. Note that in addition to an increased number of TH⁺-cell bodies, the Shh treated cells show extensive neuritic processes. Scale bar = 200 um.

Figure 3. Transport of 3H-Dopamine. The identity and functionality of the 10 surviving midbrain neurons was assessed by their ability to specifically transport dopamine. (A) Addition of 25 ng/ml Shh resulted in a 22-fold increase in 3H-DA cell uptake over controls and lower Shh concentrations. 50 ng/ml Shh gave a 30-fold 15 increase in 3H-DA uptake (error bars = s.d.) (p < 0.005 at 25 and 50 ng/ml). (B) Autoradiography was performed on sister plates to visualize dopamine transport. Only 15 cells with neuronal morphology transported 3H-DA (inset). Scale bar = 50 cpm, inset 15 m.

Figure 4. Specificity of Shh activity. (A) QC-PCR gel. Lanes 1-4 are CDNA from midbrain cultures that have been co-amplified with successive 4-fold dilutions of mimic oligo. Lane 5 is DNA marker lane. *Ptc* target is 254 bp and mimic is 100 bp(B) 20 Representative plot (corresponding to A) of the log concentration of competitive mimic versus the log of the obtained band densities of target and mimic PCR substrates demonstrates the linearity of the amplification reaction. The extrapolated value of *ptc* message in the CDNA tested is determined to be equal to the value of mimic concentration where Log Ds/Dm = 0. See main text for details of the procedure. Doses 25 in ng/ml; Ds = density of test substrate; Dm = density of competitive mimic. The r 2 value shows that determinations made within this range vary within 3%. (C) Administration of Shh induces *ptc* expression in a dose response that parallels the survival curve. The values are expressed as number of target molecules (log Ds) per 30 total amount of CDNA used in each reaction as measured by optical density at 260 nm (OD) and were determined as demonstrated in A and B. At 4 days *in vitro* Shh at 5 ng/ml increases *ptc* expression over control, and 50 ng/ml increases expression of *ptc* over the level found in the ventral mesencephalon at the time of dissection. (D) Affinity 35 purified anti-Shh antibody inhibited the Shh neurotrophic response (p < .001). Cultures were maintained for 5 days. Shh was added at a concentration of 50 ng/ml, and in the co-administration of 5 Shh and anti-Shh ("Shh antibody") Shh-was added at 0 g/ml and anti-Shh was added as a 5-fold molar excess (error bars s.e.m.).

Figure 5. Shh also supports the survival of midbrain-GABA+ neurons. (A) In addition to supporting the survival of TH+ cells in the midbrain cultures, Shh promotes the survival of GABA-immunoreactive neurons with a similar dose response (error bars=s.e.m.) (For TH, p , 0.001 at 25 and 50 ng/ml; for GABA, p < .001 at 25 and 50 ng/ml). (B) Double level immunofluorescence of SSH-treated cultures shows that the majority of the GABA+ cells (0 range) do not overlap with the TH+ cells (green); scale bar = 15 m.

Figure 6. Shh effects on striatal cultures. (A) At concentrations of 10 ng/ml and higher, Shh promotes neuronal survival as gauged by staining for tubulin PIII, and these cells are exclusively GABA+ (error bars = S.D.) (tubulin PIII, p < 0.001 at 25 and 50 ng/ml; GABA, p < .001 at 25 and 50 ng/ml). Typical fields of neurons treated with 50 ng/ml Shh stained for tubulin pIII (B) and GABA+ (C) are shown; scale bar = 100 gm.

Figure 7. Shh effects on ventral spinal cultures. (A) At concentrations of 25 ng/ml and higher, Shh promotes neuronal survival as gauged by staining for tubulin PIII. The majority of the cells stain positively for GABA, while a subset stain for the nuclear marker of spinal interneurons, Lim-1/2 (error bars = s.e.m.) (tubulin pIII, p < 0.001 at 25 and 50 ng/ml; Lim 1/2, p <.001 at 5,10,25, and 50 ng/ml; GABA, p < .001 at 25 and 50 ng/ml). Typical staining for Lim-1/2 in the E14 rat spinal cord (B, scale bar = 100 m), and spinal neurons cultured in the presence of 50 ng/ml Shh (C, scale bar = 20 m).

Figure 8. Shh protects midbrain TH+ neurons from neurotoxic insult. Cultures of ventral mesencephalon neurons were cultured in the indicated concentrations of Shh (ng/ml). MPP+ was added at 4 days *in vitro* for 48 hours. Cultures were then washed extensively and cultured for an additional 48 hours to allow clearance of dying neurons. Protection from MPP+ neurotoxicity could be seen at 5 ng/ml, with the effect saturating at 50 ng/ml. BDNF was used at 10 ng/ml, and GDNF at 20 ng/ml (error bars = s.e.m.) (Shh, p < 0.001 at 50 and 250 ng/ml; BDNF no significance; GDNF, p < .05). Note that the plating density used in this experiment was twice that used in Figure 2.

30 DETAILED DESCRIPTION OF THE INVENTION

Sonic hedgehog (*Shh*), an axis-determining secreted protein, is expressed during early vertebrate embryogenesis in the notochord and ventral neural tube. In this site it plays a role in the phenotypic specification of ventral neurons along the length of the CNS. For example, *Shh* induces the differentiation of motor neurons in the spinal cord and dopaminergic neurons in the midbrain. *Shh* expression, however, persists beyond

this induction period. We have shown here that *Shh* possesses novel activities beyond phenotype specification. Using cultures derived from the embryonic day 14.5 (E14.5) rat ventral mesencephalon, we show that *Shh* is also trophic for dopaminergic neurons. Interestingly, *Shh* not only promotes dopaminergic neuron survival, but also promotes 5 the survival of midbrain GABA-immunoeractive (GABA-ir) neurons. In cultures derived from the E15-16 striatum, *Shh* promotes the survival of GABA-ir interneurons to the exclusion of any other cell type. Cultures derived from E15-16 ventral spinal cord reveal that *Shh* is again trophic for interneurons, many of which are GABA-ir and some of which express the Lim-1/2 nuclear marker, but does not appear to support 10 motoneuron survival. *Shh* does not support survival of sympathetic or dorsal root ganglion neurons. Finally, using the midbrain cultures, we show that in the presence of MPP+, a highly specific neurotoxin, *Shh* prevents dopaminergic neuron death that normally would have occurred.

Based in part on these findings, we have determined that *Shh*, and other forms 15 of *hedgehog* proteins, are useful as protective agents in the treatment and prophylaxis for neurodegenerative disorders, particularly those resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss tissue from the substantia nigra. As described with greater detail below, exemplary disorders 20 ("candidate disorders") include Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis and the like.

The subject invention also utilizes *hedgehog* or *hedgehog* agonists as cell culture additives for the maintenance of differentiated neurons in cultures, e.g., in cultures of dopaminergic and GABA-nergic neurons. The subject methods and compositions can also be used to augment the implantation of such neuronal cells in an 25 animal.

In terms of treatment, once a patient experiences symptoms of a candidate disorder, a goal of therapy is prevention of further loss of neuron function.

I. OVERVIEW

30 The present application is directed to compositions and methods for the prevention and treatment of ischemic injury to the brain, such as resulting from stroke. The invention derives, at least in part, from the observation of a protective effect by the so called "*hedgehog*" proteins on animal stroke models. Briefly, as described in the appended examples, we investigated the neuroprotective potential of *hedgehog* proteins 35 in a rat model of focal cerebral ischemia that used permanent occlusion of the middle

5 cerebral artery. Intravenous infusion of vehicle (control) or *Shh* (sonic *hedgehog*) was administered for 3 hours beginning 30 minutes after occlusion, and resulted in a 70 percent reduction in total infarct size ($P=0.0039$), relative to the control, when examined 24 hours post-occlusion. Measurements of arterial blood pressure, blood gases, glucose, hematocrit and osmolality revealed no difference among vehicle- and *Shh*-treated animals. These results show that the intravenous *hedgehog* protein reduces neuronal damage due to stroke.

10 In one aspect, the present invention provides pharmaceutical preparations and methods for preventing/treating cerebral ischemia and the like utilizing, as an active ingredient, a *hedgehog* polypeptide or a mimetic thereof.

15 The subject *hedgehog* treatments are effective on both human and animal subjects afflicted with these conditions. Animal subjects to which the invention is applicable extend to both domestic animals and livestock, raised either as pets or for commercial purposes. Examples are dogs, cats, cattle, horses, sheep, hogs and goats.

20 25 However, without wishing to be bound by any particular theory, the reduction in infarct size in the present studies may be due at least in part to the ability of *hedgehog* proteins to antagonize (directly or indirectly) *patched*-mediated regulation of gene expression and other physiological effects mediated by the *patched* gene. The *patched* gene product, a cell surface protein, is understood to signal through a pathway which regulates transcription of a variety of genes involved in neuronal cell development. In the CNS and other tissue, the introduction of *hedgehog* relieves (derepresses) this inhibition conferred by *patched*, allowing expression of particular gene programs.

Accordingly, the present invention contemplates the use of other agents which are capable of mimicking the effect of the *hedgehog* protein on *patched* signaling, e.g., as may be identified from the drug screening assays described below.

II. DEFINITIONS

For convenience, certain terms employed in the specification, examples, and appended claims are collected here.

30 The term "hedgehog therapeutic" refers to various forms of *hedgehog* polypeptides, as well as peptidomimetics, which are neuroprotective for neuronal cells, and in particular, enhance the survival of dopaminergic and GABA-ergic neurons. These include naturally occurring forms of *hedgehog* proteins, as well as modified or mutant forms generated by molecular biological techniques, chemical synthesis, etc.

While in preferred embodiments the *hedgehog* polypeptide is derived from a vertebrate homolog, cross-species activity reported in the literature supports the use of *hedgehog* polypeptides from invertebrate organisms as well. Naturally and non-naturally occurring *hedgehog* therapeutics referred to herein as "agonists" mimic or potentiate 5 (collectively "agonize") the effects of a naturally-occurring *hedgehog* protein as a neuroprotective agent. In addition, the term "hedgehog therapeutic" includes molecules which can activate expression of an endogenous *hedgehog* gene. The term also includes gene therapy constructs for causing expression of *hedgehog* polypeptides *in vivo*, as for example, expression constructs encoding recombinant *hedgehog* 10 polypeptides as well as trans-activation constructs for altering the regulatory sequences of an endogenous *hedgehog* gene by homologous recombination.

In particular, the term "*hedgehog* polypeptide" encompasses *hedgehog* proteins and peptidyl fragments thereof.

As used herein the term "bioactive fragment", with reference to a portions of 15 *hedgehog* proteins, refers to a fragment of a full-length *hedgehog* protein, wherein the fragment specifically agonizes neuroprotective events mediated by wild-type *hedgehog* proteins. The *hedgehog* bioactive fragment preferably is a soluble extracellular portion of a *hedgehog* protein, where solubility is with reference to physiologically compatible solutions. Exemplary bioactive fragments are described in PCT publications WO 20 95/18856 and WO 96/17924.

The term "ptc therapeutic" refers to agents which mimic the effect of naturally occurring *hedgehog* proteins on *patched* signalling. The ptc therapeutic can be, e.g., a peptide, a nucleic acid, a carbohydrate, a small organic molecule, or natural product extract (or fraction thereof).

25 A "patient" or "subject" to be treated by the subject method are mammals, including humans.

An "effective amount" of, e.g., a *hedgehog* or ptc therapeutic, with respect to the subject method of treatment, refers to an amount of the therapeutic in a preparation which, when applied as part of a desired dosage regimen causes a increase in survival of 30 a neuronal cell population according to clinically acceptable standards for the treatment or prevention of a particular disorder.

By "prevent degeneration" it is meant reduction in the loss of cells (such as from apoptosis), or reduction in impairment of cell function, e.g., release of dopamine in the case of dopaminergic neurons.

A "trophic factor", referring to a *hedgehog* or *ptc* therapeutic, is a molecule that directly or indirectly affects the survival or function of a *hedgehog*-responsive cell, e.g., a dopaminergic or GABA-nergic cell.

5 A "trophic amount" of a *hedgehog* or *ptc* therapeutic is an amount sufficient to, under the circumstances, cause an increase in the rate of survival or the functional performance of a *hedgehog*-responsive cell, e.g., a dopaminergic or GABA-nergic cell.

"Homology" and "identity" each refer to sequence similarity between two polypeptide sequences, with identity being a more strict comparison. Homology and identity can each be determined by comparing a position in each sequence which may 10 be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same amino acid residue, then the polypeptides can be referred to as identical at that position; when the equivalent site is occupied by the same amino acid (e.g., identical) or a similar amino acid (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous at that position. A percentage of 15 homology or identity between sequences is a function of the number of matching or homologous positions shared by the sequences. An "unrelated" or "non-homologous" sequence shares less than 40 percent identity, though preferably less than 25 percent identity, with an AR sequence of the present invention.

20 The term "corresponds to", when referring to a particular polypeptide or nucleic acid sequence is meant to indicate that the sequence of interest is identical or homologous to the reference sequence to which it is said to correspond.

25 The terms "recombinant protein", "heterologous protein" and "exogenous protein" are used interchangeably throughout the specification and refer to a polypeptide which is produced by recombinant DNA techniques, wherein generally, DNA encoding the polypeptide is inserted into a suitable expression construct which is in turn used to transform a host cell to produce the heterologous protein. That is, the polypeptide is expressed from a heterologous nucleic acid.

30 A "chimeric protein" or "fusion protein" is a fusion of a first amino acid sequence encoding a *hedgehog* polypeptide with a second amino acid sequence defining a domain foreign to and not substantially homologous with any domain of *hh* protein. A chimeric protein may present a foreign domain which is found (albeit in a different protein) in an organism which also expresses the first protein, or it may be an "interspecies", "intergenic", etc. fusion of protein structures expressed by different kinds of organisms. In general, a fusion protein can be represented by the general 35 formula (X)_n-(*hh*)_m-(Y)_n, wherein *hh* represents all or a portion of the *hedgehog*

protein, X and Y each independently represent an amino acid sequences which are not naturally found as a polypeptide chain contiguous with the *hedgehog* sequence, m is an integer greater than or equal to 1, and each occurrence of n is, independently, 0 or an integer greater than or equal to 1 (n and m are preferably no greater than 5 or 10).

5 As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. The term "expression vector" includes plasmids, cosmids or phages capable of synthesizing, for example, the subject *hedgehog* polypeptides encoded by the respective recombinant gene carried by the vector. Preferred vectors are those capable of autonomous replication

10 and/expression of nucleic acids to which they are linked. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. Moreover, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

15 "Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, as well as polyadenylation sites, which induce or control transcription of protein (or antisense) coding sequences with which they are operably linked. In preferred embodiments, transcription of a recombinant gene is under the control of a

20 promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring form of the

25 regulatory protein.

30 The term "operably linked" refers to the arrangement of a transcriptional regulatory element relative to other transcribable nucleic acid sequence such that the transcriptional regulatory element can regulate the rate of transcription from the transcribable sequence(s).

30

III. EXEMPLARY APPLICATIONS OF METHOD AND COMPOSITIONS

35 One aspect of the present invention relates to a method of maintaining a differentiated state, e.g., enhancing survival, of a neuronal cell responsive to a *hedgehog* protein, by contacting the cells with a trophic amount of a hedgehog or ptc therapeutic. For instance, it is contemplated by the invention that, in light of the

present finding of an apparently trophic effect of *hedgehog* proteins in the maintenance of differentiated neurons, the subject method could be used to maintain different neuronal tissue both *in vitro* and *in vivo*. Where the trophic agent is a *hedgehog* protein, it can be provided to a cell culture or animal as a purified protein or secreted by

5 a recombinant cell, or cells or tissue explants which naturally produce one or more *hedgehog* proteins. For instance, neural tube explants from embryos, particularly floorplate tissue, can provide a source for *Shh* polypeptide, which source can be implanted in a patient or otherwise provided, as appropriate, for maintenance of differentiation.

10 The present method is applicable to cell culture techniques. *In vitro* neuronal culture systems have proved to be fundamental and indispensable tools for the study of neural development, as well as the identification of neurotrophic factors such as nerve growth factor (NGF), ciliary trophic factors (CNTF), and brain derived neurotrophic factor (BDNF). Once a neuronal cell has become terminally-differentiated it typically

15 will not change to another terminally differentiated cell-type. However, neuronal cells can nevertheless readily lose their differentiated state. This is commonly observed when they are grown in culture from adult tissue, and when they form a blastema during regeneration. The present method provides a means for ensuring an adequately restrictive environment in order to maintain dopaminergic and GABA-nergic cells in

20 differentiated states, and can be employed, for instance, in cell cultures designed to test the specific activities of other trophic factors.

In such embodiments of the subject method, a culture of differentiated cells including dopaminergic and/or GABA-nergic cells can be contacted with a *hedgehog* or ptc therapeutic in order to maintain the integrity of a culture of terminally-differentiated

25 neuronal cells by preventing loss of differentiation. The source of *hedgehog* or ptc therapeutic in the culture can be derived from, for example, a purified or semi-purified protein composition added directly to the cell culture media, or alternatively, supported and/or released from a polymeric device which supports the growth of various neuronal cells and which has been doped with the protein. The source of, for example, a trophic

30 *hedgehog* polypeptide can also be a cell that is co-cultured with the neuronal cells. Alternatively, the source can be the neuronal cell itself which has been engineered to produce a recombinant *hedgehog* protein. Such neuronal cultures can be used as convenient assay systems as well as sources of implantable cells for therapeutic treatments.

The subject method can be used in conjunction with agents which induce the differentiation of neuronal precursors, e.g., progenitor or stem cells, into dopaminergic or GABA-nergic neurons.

Cells can be obtained from embryonic, post-natal, juvenile or adult neural tissue 5 from any animal. By any animal is meant any multicellular animal which contains nervous tissue. More particularly, is meant any fish, reptile, bird, amphibian or mammal and the like. The most preferable donors are mammals, especially humans and non-human primates, pigs, cows, and rodents.

Intracerebral neural grafting has emerged recently as an additional potential to 10 CNS therapy. For example, one approach to repairing damaged brain tissues involves the transplantation of cells from fetal or neonatal animals into the adult brain (Dunnett et al. (1987) *J Exp Biol* 123:265-289; and Freund et al. (1985) *J Neurosci* 5:603-616). Fetal neurons from a variety of brain regions can be successfully incorporated into the 15 adult brain, and such grafts can alleviate behavioral defects. For example, movement disorder induced by lesions of dopaminergic projections to the basal ganglia can be prevented by grafts of embryonic dopaminergic neurons. Complex cognitive functions that are impaired after lesions of the neocortex can also be partially restored by grafts of embryonic cortical cells. Transplantation of fetal brain cells, which contain precursors 20 of the dopaminergic neurons, has been examined with success as a treatment for Parkinson's disease. In animal models and in patients with this disease, fetal brain cell transplantations have resulted in the reduction of motor abnormalities. Furthermore, it appears that the implanted fetal dopaminergic neurons form synapses with surrounding 25 host neurons. However, in the art, the transplantation of fetal brain cells is limited due, for example, to the limited survival time of the implanted neuronal precursors and differentiated neurons arising therefrom. The subject invention provides a means for extending the usefulness of such transplants by enhancing the survival of dopaminergic and/or GABA-nergic cells in the transplant.

In the specific case of Parkinson's disease, intervention by increasing the 30 activity of *hedgehog*, by ectopic or endogenous means, can improve the *in vivo* survival of fetal and adult dopaminergic neurons, and thus can provide a more effective treatment of this disease. Cells to be transplanted for the treatment of a particular disease can be genetically modified *in vitro* so as to increase the expression of *hedgehog* in the transplant. In an exemplary embodiment of the invention, 35 administration of an *Shh* polypeptide can be used in conjunction with surgical implantation of tissue in the treatment of Parkinson's disease.

In the case of a heterologous donor animal, the animal may be euthanized, and the brain and specific area of interest removed using a sterile procedure. Brain areas of particular interest include any area from which progenitor cells can be obtained which will provide dopaminergic or GABA-nergic cells upon differentiation. These regions 5 include areas of the central nervous system (CNS) including the substantia nigra pars compacta which is found to be degenerated in Parkinson's Disease patients.

Human heterologous neural progenitor cells may be derived from fetal tissue obtained from elective abortion, or from a post-natal, juvenile or adult organ donor. Autologous neural tissue can be obtained by biopsy, or from patients undergoing 10 neurosurgery in which neural tissue is removed, such as during epilepsy surgery.

Cells can be obtained from donor tissue by dissociation of individual cells from the connecting extracellular matrix of the tissue. Dissociation can be obtained using any known procedure, including treatment with enzymes such as trypsin, collagenase and the like, or by using physical methods of dissociation such as with a blunt 15 instrument. Dissociation of fetal cells can be carried out in tissue culture medium, while a preferable medium for dissociation of juvenile and adult cells is artificial cerebral spinal fluid (aCSF). Regular aCSF contains 124 mM NaCl, 5 mM KCl, 1.3 mM MgCl₂, 2 mM CaCl₂, 26 mM NaHCO₃, and 10 mM D-glucose. Low Ca²⁺ aCSF contains the same ingredients except for MgCl₂ at a concentration of 3.2 mM and 20 CaCl₂ at a concentration of 0.1 mM.

Dissociated cells can be placed into any known culture medium capable of supporting cell growth, including MEM, DMEM, RPMI, F-12, and the like, containing supplements which are required for cellular metabolism such as glutamine and other amino acids, vitamins, minerals and useful proteins such as transferrin and the like. 25 Medium may also contain antibiotics to prevent contamination with yeast, bacteria and fungi such as penicillin, streptomycin, gentamicin and the like. In some cases, the medium may contain serum derived from bovine, equine, chicken and the like. A particularly preferable medium for cells is a mixture of DMEM and F-12.

Conditions for culturing should be close to physiological conditions. The pH of 30 the culture media should be close to physiological pH, preferably between pH 6-8, more preferably close to pH 7, even more particularly about pH 7.4. Cells should be cultured at a temperature close to physiological temperature, preferably between 30°C-40°C, more preferably between 32°C-38°C, and most preferably between 35°C-37°C.

Cells can be grown in suspension or on a fixed substrate, but proliferation of the progenitors is preferably done in suspension to generate large numbers of cells by formation of "neurospheres" (see, for example, Reynolds et al. (1992) *Science* 255:1070-1079; and PCT Publications WO93/01275, WO94/09119, WO94/10292, and 5 WO94/16718). In the case of propagating (or splitting) suspension cells, flasks are shaken well and the neurospheres allowed to settle on the bottom corner of the flask. The spheres are then transferred to a 50 ml centrifuge tube and centrifuged at low speed. The medium is aspirated, the cells resuspended in a small amount of medium with growth factor, and the cells mechanically dissociated and resuspended in separate 10 aliquots of media.

Cell suspensions in culture medium are supplemented with any growth factor which allows for the proliferation of progenitor cells and seeded in any receptacle capable of sustaining cells, though as set out above, preferably in culture flasks or roller bottles. Cells typically proliferate within 3-4 days in a 37°C incubator, and 15 proliferation can be reinitiated at any time after that by dissociation of the cells and resuspension in fresh medium containing growth factors.

In the absence of substrate, cells lift off the floor of the flask and continue to proliferate in suspension forming a hollow sphere of undifferentiated cells. After approximately 3-10 days *in vitro*, the proliferating clusters (neurospheres) are fed every 20 2-7 days, and more particularly every 2-4 days by gentle centrifugation and resuspension in medium containing growth factor.

After 6-7 days *in vitro*, individual cells in the neurospheres can be separated by physical dissociation of the neurospheres with a blunt instrument, more particularly by triturating the neurospheres with a pipette. Single cells from the dissociated 25 neurospheres are suspended in culture medium containing growth factors, and differentiation of the cells can be induced by plating (or resuspending) the cells in the presence of a factor capable of sustaining differentiation, e.g., such as a *hedgehog* or *ptc* therapeutic of the present invention.

Stem cells useful in the present invention are generally known. For example, 30 several neural crest cells have been identified, some of which are multipotent and likely represent uncommitted neural crest cells. The role of *hedgehog* proteins employed in the present method to culture such stem cells is to maintain differentiation a committed progenitor cell and/or a terminally-differentiated dopaminergic or GABA-nergic neuronal cell. The *hedgehog* protein can be used alone, or can be used in combination

with other neurotrophic factors which act to more particularly enhance a particular differentiation fate of the neuronal progenitor cell.

In addition to the implantation of cells cultured in the presence of a functional *hedgehog* activity and other *in vitro* uses described above, yet another aspect of the 5 present invention concerns the therapeutic application of a *hedgehog* or ptc therapeutic to enhance survival of dopaminergic and GABA-nergic neurons *in vivo*. The ability of *hedgehog* protein to maintain dopaminergic and GABA-nergic neuronal differentiation indicates that certain of the *hedgehog* proteins can be reasonably expected to facilitate control of these neuronal cell-types in adult tissue with regard to maintenance, 10 functional performance, aging and prevention of degeneration and premature death which result from loss of differentiation in certain pathological conditions. In light of this understanding, the present invention specifically contemplates applications of the subject method to the treatment of (prevention and/or reduction of the severity of) 15 neurological conditions deriving from (i) loss of dopaminergic cells, (ii) loss of GABA-nergic cells, and/or (iii) loss of neurons of the substantia nigra. In this regard, the subject method is useful in the treatment of chronic neurodegenerative diseases of the nervous system, including Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis and the like.

Many neurological disorders are associated with degeneration of discrete 20 populations of neuronal elements and may be treatable with a therapeutic regimen which includes a *hedgehog* or ptc therapeutic according to the subject invention. As described in the appended examples, *hedgehog* exerts trophic and survival-promoting actions on substantia nigra dopaminergic neurons. *In vivo*, treatment with exogenous *hedgehog*, or other compounds of the present invention, is expected to stimulate the 25 dopaminergic phenotype of substantia nigra neurons and restores functional deficits induced by axotomy or dopaminergic neurotoxins, and may be used the treatment of Parkinson's disease, a neurodegenerative disease characterized by the loss of dopaminergic neurons. Thus, in one embodiment, the subject method comprises administering to an animal affected with Parkinson's disease, or at risk of developing 30 Parkonson's disease, an amount of a *hedgehog* or ptc thereapeutic effective for increasing the rate of survival of dopaminergic neurons in the animal. In preferred embodiments, the method includes administering to the animal an amount of a *hedgehog* or ptc thereapeutic which would otherwise be effective at protecting the substantia nigra from MPTP-mediated toxicity when MPTP is administered at a dose of 35 .5mg/kg, more preferably at a dose of 2mg/kg, 5mg/kg, 10mg/kg, 20mg/kg or 50mg/kg and, more preferably, at a dose of 100mg/kg.

Huntington's disease involves the degeneration of intrastralial and cortical cholinergic neurons and GABA-nergic neurons. Treatment of patients suffering from such degenerative conditions can include the application of *hedgehog* or *ptc* therapeutics of the present invention, in order to control, for example, apoptotic events 5 which give rise to loss of GABA-nergic neurons (e.g. to enhance survival of existing neurons).

Recently it has been reported that in certain ALS patients and animal models a significant loss of midbrain dopaminergic neurons occurs in addition to the loss of spinal motor neurons. For instance, the literature describes degeneration of the 10 substantia nigra in some patients with familial amyotrophic lateral sclerosis. Kostic et al. (1997) Ann Neurol 41:497-504. According the subject invention, a trophic amount of a *hedgehog* or *ptc* therapeutic can be administered to an animal suffering from, or at risk of developing, ALS.

In general, the therapeutic method of the present invention can be characterized 15 as including a step of administering to an animal an amount of a *ptc* or *hedgehog* therapeutic effective to enhance the survival of a dopaminergic and/or GABA-nergic neuronal cells. The mode of administration and dosage regimens will vary depending on the severity of the degenerative disorder being treated, e.g., the dosage may be altered as between a prophylaxis and treatment. In preferred embodiments, the *ptc* or hedgehog 20 therapeutic is administered systemically initially, then locally for medium to long term care. In certain embodiments, a source of a *hedgehog* or *ptc* therapeutic is stereotactically provided within or proximate the area of degeneration.

The subject method may also find particular utility in treating or preventing the 25 adverse neurological consequences of surgery. For example, certain cranial surgery can result in degeneration of neuronal populations for which the subject method can be applied.

In other embodiments, the subject method can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, such as the compound MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine).

30 In still other embodiments, the subject method can be used in the prevention and/or treatment of hypoxia, e.g., as a neuroprotective agent. For instance, the subject method can be used prophylactically to lessen the neuronal cell death caused by altitude-induced hypoxia.

A method which is "neuroprotective", in the case of dopaminergic and GABA-nergic cells, results in diminished loss of cells of those phenotype relative to that which would occur in the absence of treatment with a *hedgehog* or *ptc* therapeutic.

In yet other embodiments, the subject method can be carried out conjointly with 5 the administration of growth and/or trophic factors. For instance, the combinatorial therapy can include a trophic factor such as nerve growth factor, ciliary neurotrophic growth factor, schwannoma-derived growth factor, glial growth factor, stiatal-derived neuronotrophic factor, platelet-derived growth factor, and scatter factor (HGF-SF). Antimitogenic agents can also be used, as for example, cytosine, arabinoside, 5- 10 fluorouracil, hydroxyurea, and methotrexate.

Determination of a therapeutically effective amount and a prophylactically effective amount of a *hedgehog* or *ptc* therapeutic, e.g., to be adequately neuroprotective, can be readily made by the physician or veterinarian (the "attending clinician"), as one skilled in the art, by the use of known techniques and by observing 15 results obtained under analogous circumstances. The dosages may be varied depending upon the requirements of the patient in the judgment of the attending clinician, the severity of the condition being treated, the risk of further degeneration to the CNS, and the particular agent being employed. In determining the therapeutically effective trophic amount or dose, and the prophylactically effective amount or dose, a number of factors 20 are considered by the attending clinician, including, but not limited to: the specific cause of the degenerative state and its likelihood of recurring or worsening; pharmacodynamic characteristics of the particular agent and its mode and route of administration; the desirder time course of treatment; the species of mammal; its size, age, and general health; the response of the individual patient; the particular compound 25 administered; the bioavailability characteristics of the preparation administered; the dose regimen selected; the kind of concurrent treatment (i.e., the interaction of the *hedgehog* or *ptc* therapeutic with other co-administered therapeutics); and other relevant circumstances.

Treatment can be initiated with smaller dosages which are less than the 30 optimum dose of the agent. Thereafter, the dosage should be increased by small increments until the optimum effect under the circumstances is reached. For convenience, the total daily dosage may be divided and administered in portions during the day if desired. A therapeutically effective trophic amount and a prophylactically effective neuroprotective amount of a *hedgehog* polypeptide, for instance, is expected 35 to vary from concentrations about 0.1 nanogram per kilogram of body weight per day (ng/kg/day) to about 100 mg/kg/day.

Potential *hedgehog* and *ptc* therapeutics, such as described below, can be tested by any of number of well known animal disease models. For instance, regarding Parkinson's Disease, selected agents can be evaluated in animals treated with MPTP. The compound MPTP (1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine) and its 5 metabolite MPP⁺ have been used to induce experimental parkinsonism. MPP⁺ kills dopaminergic neurons in the substantia nigra, yielding a reasonable model of late parkinsonism. Turski et al., (1991) *Nature* 349:414.

Compounds which are determined to be effective for the prevention or treatment of degeneration of dopaminergic and GABA-nergic neurons and the like in animals, 10 e.g., dogs, rodents, may also be useful in treatment of disorders in humans. Those skilled in the art of treating in such disorders in humans will be guided, from the data obtained in animal studies, to the correct dosage and route of administration of the compound to humans. In general, the determination of dosage and route of administration in humans is expected to be similar to that used to determine 15 administration in animals.

The identification of those patients who are in need of prophylactic treatment for disorders marked by degeneration of dopaminergic and/or GABA-nergic neurons is well within the ability and knowledge of one skilled in the art. Certain of the methods for identification of patients which are at risk and which can be treated by the subject 20 method are appreciated in the medical arts, such as family history of the development of a particular disease state and the presence of risk factors associated with the development of that disease state in the subject patient. A clinician skilled in the art can readily identify such candidate patients, by the use of, for example, clinical tests, physical examination and medical/family history.

25

IV. EXEMPLARY HEDGEHOG THERAPEUTIC COMPOUNDS:

The *hedgehog* therapeutic compositions of the subject method can be generated by any of a variety of techniques, including purification of naturally occurring proteins, recombinantly produced proteins and synthetic chemistry. Polypeptide forms of the 30 *hedgehog* therapeutics are preferably derived from vertebrate *hedgehog* proteins, e.g., have sequences corresponding to naturally occurring *hedgehog* proteins, or fragments thereof, from vertebrate organisms. However, it will be appreciated that the *hedgehog* polypeptide can correspond to a *hedgehog* protein (or fragment thereof) which occurs in any metazoan organism.

The various naturally-occurring *hedgehog* proteins from which the subject therapeutics can be derived are characterized by a signal peptide, a highly conserved N-terminal region, and a more divergent C-terminal domain. In addition to signal sequence cleavage in the secretory pathway (Lee, J.J. *et al.* (1992) *Cell* 71:33-50; 5 Tabata, T. *et al.* (1992) *Genes Dev.* 2635-2645; Chang, D.E. *et al.* (1994) *Development* 120:3339-3353), *hedgehog* precursor proteins naturally undergo an internal autoproteolytic cleavage which depends on conserved sequences in the C-terminal portion (Lee *et al.* (1994) *Science* 266:1528-1537; Porter *et al.* (1995) *Nature* 374:363-10 366). This autocleavage leads to a 19 kD N-terminal peptide and a C-terminal peptide of 26-28 kD (Lee *et al.* (1992) *supra*; Tabata *et al.* (1992) *supra*; Chang *et al.* (1994) *supra*; Lee *et al.* (1994) *supra*; Bumcrot, D.A., *et al.* (1995) *Mol. Cell. Biol.* 15:2294-15 2303; Porter *et al.* (1995) *supra*; Ekker, S.C. *et al.* (1995) *Curr. Biol.* 5:944-955; Lai, C.J. *et al.* (1995) *Development* 121:2349-2360). The N-terminal peptide stays tightly associated with the surface of cells in which it was synthesized, while the C-terminal peptide is freely diffusible both *in vitro* and *in vivo* (Lee *et al.* (1994) *supra*; Bumcrot *et al.* (1995) *supra*; Mart', E. *et al.* (1995) *Development* 121:2537-2547; Roelink, H. *et al.* (1995) *Cell* 81:445-455). Cell surface retention of the N-terminal peptide is dependent 20 on autocleavage, as a truncated form of *hedgehog* encoded by an RNA which terminates precisely at the normal position of internal cleavage is diffusible *in vitro* (Porter *et al.* (1995) *supra*) and *in vivo* (Porter, J.A. *et al.* (1996) *Cell* 86, 21-34). Biochemical studies have shown that the autoproteolytic cleavage of the *hedgehog* precursor protein proceeds through an internal thioester intermediate which subsequently is cleaved in a nucleophilic substitution. It is suggested that the nucleophile is a small lipophilic molecule, more particularly cholesterol, which 25 becomes covalently bound to the C-terminal end of the N-peptide (Porter *et al.* (1996) *supra*), tethering it to the cell surface.

The vertebrate family of *hedgehog* genes includes at least four members, e.g., 30 paralogs of the single *drosophila* *hedgehog* gene (SEQ ID No. 19). Three of these members, herein referred to as *Desert hedgehog* (*Dhh*), *Sonic hedgehog* (*Shh*) and *Indian hedgehog* (*Ihh*), apparently exist in all vertebrates, including fish, birds, and mammals. A fourth member, herein referred to as *tiggle-winkle hedgehog* (*Thh*), appears specific to fish. According to the appended sequence listing, (see also Table 1) 35 a chicken *Shh* polypeptide is encoded by SEQ ID No:1; a mouse *Dhh* polypeptide is encoded by SEQ ID No:2; a mouse *Ihh* polypeptide is encoded by SEQ ID No:3; a mouse *Shh* polypeptide is encoded by SEQ ID No:4 a zebrafish *Shh* polypeptide is encoded by SEQ ID No:5; a human *Shh* polypeptide is encoded by SEQ ID No:6; a

human *Ihh* polypeptide is encoded by SEQ ID No:7; a human *Dhh* polypeptide is encoded by SEQ ID No. 8; and a zebrafish *Thh* is encoded by SEQ ID No. 9.

5

Table 1
Guide to *hedgehog* sequences in Sequence Listing

	Nucleotide	Amino Acid
Chicken <i>Shh</i>	SEQ ID No. 1	SEQ ID No. 10
Mouse <i>Dhh</i>	SEQ ID No. 2	SEQ ID No. 11
Mouse <i>Ihh</i>	SEQ ID No. 3	SEQ ID No. 12
Mouse <i>Shh</i>	SEQ ID No. 4	SEQ ID No. 13
Zebrafish <i>Shh</i>	SEQ ID No. 5	SEQ ID No. 14
Human <i>Shh</i>	SEQ ID No. 6	SEQ ID No. 15
Human <i>Ihh</i>	SEQ ID No. 7	SEQ ID No. 16
Human <i>Dhh</i>	SEQ ID No. 8	SEQ ID No. 17
Zebrafish <i>Thh</i>	SEQ ID No. 9	SEQ ID No. 18
Drosophila <i>HH</i>	SEQ ID No. 19	SEQ ID No. 20

In addition to the sequence variation between the various *hedgehog* homologs, the *hedgehog* proteins are apparently present naturally in a number of different forms, 10 including a pro-form, a full-length mature form, and several processed fragments thereof. The pro-form includes an N-terminal signal peptide for directed secretion of the extracellular domain, while the full-length mature form lacks this signal sequence.

As described above, further processing of the mature form occurs in some instances to yield biologically active fragments of the protein. For instance, *sonic hedgehog* undergoes additional proteolytic processing to yield two peptides of 15 approximately 19 kDa and 27 kDa, the 19kDa fragment corresponding to a proteolytic N-terminal portion of the mature protein. In addition to proteolytic fragmentation, the vertebrate *hedgehog* proteins can also be modified post-translationally, such as by glycosylation and/or addition of sterols (e.g., cholesterol), though bacterially produced 20 (e.g. unglycosylated/uncholesterolized) forms of the proteins still maintain certain of the bioactivities of the native protein. Bioactive fragments of *hedgehog* polypeptides of the present invention have been generated and are described in great detail in, e.g., PCT publications WO 95/18856 and WO 96/17924.

Moreover, mutagenesis can be used to create modified *hh* polypeptides, e.g., for 25 such purposes as enhancing therapeutic or prophylactic efficacy, or stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation *in vivo*). Such modified

peptides can be produced, for instance, by amino acid substitution, deletion, or addition. Modified *hedgehog* polypeptides can also include those with altered post-translational processing relative to a naturally occurring *hedgehog* protein, e.g., altered glycosylation, choleresterolization, prenylation and the like.

5 In one embodiment, the *hedgehog* therapeutic is a polypeptide encodable by a nucleotide sequence that hybridizes under stringent conditions to a *hedgehog* coding sequence represented in one or more of SEQ ID Nos:1-9 or 19. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C,
10 are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room
15 temperature, about 22°C, to high stringency conditions at about 65°C.

As described in the literature, genes for other *hedgehog* proteins, e.g., from other animals, can be obtained from mRNA or genomic DNA samples using techniques well known in the art. For example, a cDNA encoding a *hedgehog* protein can be obtained by isolating total mRNA from a cell, e.g. a mammalian cell, e.g. a human cell,
20 including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene encoding a *hedgehog* protein can also be cloned using established polymerase chain reaction techniques.

Preferred nucleic acids encode a *hedgehog* polypeptide comprising an amino acid sequence at least 60% homologous, more preferably 70% homologous and most preferably 80% homologous with an amino acid sequence selected from the group consisting of SEQ ID Nos:8-14. Nucleic acids which encode polypeptides at least about 90%, more preferably at least about 95%, and most preferably at least about 98-99% homology with an amino acid sequence represented in one of SEQ ID Nos:10-18 or 20
30 are also within the scope of the invention.

Hedgehog polypeptides preferred by the present invention, in addition to native *hedgehog* proteins, are at least 60% homologous, more preferably 70% homologous and most preferably 80% homologous with an amino acid sequence represented by any of SEQ ID Nos:10-18 or 20. Polypeptides which are at least 90%, more preferably at least 95%, and most preferably at least about 98-99% homologous with a sequence
35

selected from the group consisting of SEQ ID Nos:10-18 or 20 are also within the scope of the invention. The only prerequisite is that the *hedgehog* polypeptide is capable of protecting neuronal cells against degeneration, e.g., the polypeptide is trophic for a dopaminergic and/or GABA-nergic neuron.

5 The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a *hedgehog* polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant *hedgehog* gene, is meant to include 10 within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native *hedgehog* protein, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the protein.

15 The method of the present invention can also be carried out using variant forms of the naturally occurring *hedgehog* polypeptides, e.g., mutational variants.

As is known in the art, *hedgehog* polypeptides can be produced by standard biological techniques. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. The 20 polypeptide *hedgehog* may be secreted and isolated from a mixture of cells and medium containing the recombinant *hedgehog* polypeptide. Alternatively, the peptide may be retained cytoplasmically by removing the signal peptide sequence from the recombinant *hedgehog* gene and the cells harvested, lysed and the protein isolated. A cell culture includes host cells, media and other byproducts. Suitable media for cell culture are well 25 known in the art. The recombinant *hedgehog* polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred embodiment, the recombinant *hedgehog* polypeptide is 30 a fusion protein containing a domain which facilitates its purification, such as an *hedgehog*/GST fusion protein. The host cell may be any prokaryotic or eukaryotic cell.

Recombinant *hedgehog* genes can be produced by ligating nucleic acid encoding an *hedgehog* protein, or a portion thereof, into a vector suitable for expression in either prokaryotic cells, eukaryotic cells, or both. Expression vectors for production of 35 recombinant forms of the subject *hedgehog* polypeptides include plasmids and other

vectors. For instance, suitable vectors for the expression of a *hedgehog* polypeptide include plasmids of the types: pBR322-derived plasmids, pEMBL-derived plasmids, pEX-derived plasmids, pBTac-derived plasmids and pUC-derived plasmids for expression in prokaryotic cells, such as *E. coli*.

5 A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into *S. cerevisiae* (see, for example, Broach *et al.* (1983) in *Experimental Manipulation of Gene Expression*, ed. M. Inouye Academic Press, p. 83, incorporated by reference herein).

10 These vectors can replicate in *E. coli* due the presence of the pBR322 ori, and in *S. cerevisiae* due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, an *hedgehog* polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning the coding sequence of one of the *hedgehog* genes represented

15 in SEQ ID Nos:1-9 or 19.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The pcDNA1/amp, pcDNA1/neo, pRc/CMV, pSV2gpt, pSV2neo, pSV2-dhfr, pTk2, pRSVneo, pMSG, pSVT7, pko-neo and pHg derived vectors are examples of mammalian expression vectors suitable for transfection of eukaryotic cells. Some of these vectors are modified with sequences from bacterial plasmids, such as pBR322, to facilitate replication and drug resistance selection in both prokaryotic and eukaryotic cells. Alternatively, derivatives of viruses such as the bovine papillomavirus (BPV-1), or Epstein-Barr virus (pHEBo, pREP-derived and p205) can be used for transient expression of proteins in eukaryotic cells. The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

In some instances, it may be desirable to express the recombinant *hedgehog* polypeptide by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the β -gal containing pBlueBac III).

When it is desirable to express only a portion of a *hedgehog* protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a 5 methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat et al. (1987) *J. Bacteriol.* 169:751-757) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller et al. (1987) *PNAS* 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be 10 achieved either *in vivo* by expressing *hedgehog*-derived polypeptides in a host which produces MAP (e.g., *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP (e.g., procedure of Miller et al., *supra*).

Alternatively, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. 15 It is widely appreciated that fusion proteins can also facilitate the expression of proteins, and accordingly, can be used in the expression of the *hedgehog* polypeptides of the present invention. For example, *hedgehog* polypeptides can be generated as glutathione-S-transferase (GST-fusion) proteins. Such GST-fusion proteins can enable easy purification of the *hedgehog* polypeptide, as for example by the use of glutathione- 20 derivatized matrices (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. (N.Y.: John Wiley & Sons, 1991)). In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence, can be used to replace the signal sequence which naturally occurs at the N-terminus of the *hedgehog* protein (e.g. of the pro-form, in order to permit 25 purification of the poly(His)-*hedgehog* protein by affinity chromatography using a Ni²⁺ metal resin. The purification leader sequence can then be subsequently removed by treatment with enterokinase (e.g., see Hochuli et al. (1987) *J. Chromatography* 411:177; and Janknecht et al. *PNAS* 88:8972).

Techniques for making fusion genes are known to those skilled in the art. 30 Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, 35 the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried

out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. John Wiley & Sons: 1992).

5 *Hedgehog* polypeptides may also be chemically modified to create *hedgehog* derivatives by forming covalent or aggregate conjugates with other chemical moieties, such as glycosyl groups, cholesterol, isoprenoids, lipids, phosphate, acetyl groups and the like. Covalent derivatives of *hedgehog* proteins can be prepared by linking the chemical moieties to functional groups on amino acid sidechains of the protein or at the
10 N-terminus or at the C-terminus of the polypeptide.

For instance, *hedgehog* proteins can be generated to include a moiety, other than sequence naturally associated with the protein, that binds a component of the extracellular matrix and enhances localization of the analog to cell surfaces. For example, sequences derived from the fibronectin "type-III repeat", such as a tetrapeptide
15 sequence R-G-D-S (Pierschbacher et al. (1984) *Nature* 309:30-3; and Kornblhtt et al. (1985) *EMBO* 4:1755-9) can be added to the *hedgehog* polypeptide to support attachment of the chimeric molecule to a cell through binding ECM components (Ruoslahti et al. (1987) *Science* 238:491-497; Pierschbacher et al. (1987) *J. Biol. Chem.* 262:17294-8.; Hynes (1987) *Cell* 48:549-54; and Hynes (1992) *Cell* 69:11-25).

20 In preferred embodiment, the *hedgehog* polypeptide is isolated from, or is otherwise substantially free of, other cellular proteins, especially other extracellular or cell surface associated proteins which may normally be associated with the *hedgehog* polypeptide. The term "substantially free of other cellular or extracellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified
25 preparations" are defined as encompassing preparations of *hedgehog* polypeptides having less than 20% (by dry weight) contaminating protein, and preferably having less than 5% contaminating protein. By "purified", it is meant that the indicated molecule is present in the substantial absence of other biological macromolecules, such as other proteins. The term "purified" as used herein preferably means at least 80% by dry
30 weight, more preferably in the range of 95-99% by weight, and most preferably at least 99.8% by weight, of biological macromolecules of the same type present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 5000, can be present). The term "pure" as used herein preferably has the same numerical limits as "purified" immediately above.

As described above for recombinant polypeptides, isolated *hedgehog* polypeptides can include all or a portion of the amino acid sequences represented in any of SEQ ID Nos:10-18 or 20, or a homologous sequence thereto. Preferred fragments of the subject *hedgehog* proteins correspond to the N-terminal and C-terminal proteolytic 5 fragments of the mature protein. Bioactive fragments of *hedgehog* polypeptides are described in great detail in PCT publications WO 95/18856 and WO 96/17924.

With respect to bioactive fragments of *hedgehog* polypeptide, preferred *hedgehog* therapeutics include at least 50 amino acid residues of a *hedgehog* polypeptide, more preferably at least 100, and even more preferably at least 150.

10 Another preferred *hedgehog* polypeptide which can be included in the *hedgehog* therapeutic is an N-terminal fragment of the mature protein having a molecular weight of approximately 19 kDa.

Preferred human *hedgehog* proteins include N-terminal fragments corresponding approximately to residues 24-197 of SEQ ID No. 15, 28-202 of SEQ ID 15 No. 16, and 23-198 of SEQ ID No. 17. By "corresponding approximately" it is meant that the sequence of interest is at most 20 amino acid residues different in length to the reference sequence, though more preferably at most 5, 10 or 15 amino acid different in length.

20 Still other preferred *hedgehog* polypeptides includes an amino acid sequence represented by the formula A-B wherein: (i) A represents all or the portion of the amino acid sequence designated by residues 1-168 of SEQ ID No:21; and B represents at least one amino acid residue of the amino acid sequence designated by residues 169-221 of SEQ ID No:21; (ii) A represents all or the portion of the amino acid sequence designated by residues 24-193 of SEQ ID No:15; and B represents at least one amino acid residue of the amino acid sequence designated by residues 194-250 of SEQ ID 25 No:15; (iii) A represents all or the portion of the amino acid sequence designated by residues 25-193 of SEQ ID No:13; and B represents at least one amino acid residue of the amino acid sequence designated by residues 194-250 of SEQ ID No:13; (iv) A represents all or the portion of the amino acid sequence designated by residues 23-193 30 of SEQ ID No:11; and B represents at least one amino acid residue of the amino acid sequence designated by residues 194-250 of SEQ ID No:11; (v) A represents all or the portion of the amino acid sequence designated by residues 28-197 of SEQ ID No:12; and B represents at least one amino acid residue of the amino acid sequence designated by residues 198-250 of SEQ ID No:12; (vi) A represents all or the portion of the amino acid sequence designated by residues 29-197 of SEQ ID No:16; and B represents at 35

least one amino acid residue of the amino acid sequence designated by residues 198-250 of SEQ ID No:16; or (vii) A represents all or the portion of the amino acid sequence designated by residues 23-193 of SEQ ID No. 17, and B represents at least one amino acid residue of the amino acid sequence designated by residues 194-250 of 5 SEQ ID No. 17. In certain preferred embodiments, A and B together represent a contiguous polypeptide sequence designated sequence, A represents at least 25, 50, 75, 100, 125 or 150 amino acids of the designated sequence, and B represents at least 5, 10, or 20 amino acid residues of the amino acid sequence designated by corresponding entry in the sequence listing, and A and B together preferably represent a contiguous 10 sequence corresponding to the sequence listing entry. Similar fragments from other *hedgehog* also contemplated, e.g., fragments which correspond to the preferred fragments from the sequence listing entries which are enumerated above.

Isolated peptidyl portions of *hedgehog* proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid 15 encoding such peptides. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a *hedgehog* polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can 20 be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as agonists of a wild-type (e.g., "authentic") *hedgehog* protein. For example, Román et al. (1994) *Eur J Biochem* 222:65-73 describe the use of competitive-binding assays using short, overlapping synthetic peptides from larger proteins to identify binding domains.

25 The recombinant *hedgehog* polypeptides of the present invention also include homologs of the authentic *hedgehog* proteins, such as versions of those protein which are resistant to proteolytic cleavage, as for example, due to mutations which alter potential cleavage sequences or which inactivate an enzymatic activity associated with the protein. *Hedgehog* homologs of the present invention also include proteins which 30 have been post-translationally modified in a manner different than the authentic protein. Exemplary derivatives of *hedgehog* proteins include polypeptides which lack glycosylation sites (e.g. to produce an unglycosylated protein), which lack sites for cholerolization, and/or which lack N-terminal and/or C-terminal sequences.

35 Modification of the structure of the subject *hedgehog* polypeptides can also be for such purposes as enhancing therapeutic or prophylactic efficacy, or stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation *in vivo*). Such modified

peptides, when designed to retain at least one activity of the naturally-occurring form of the protein, are considered functional equivalents of the *hedgehog* polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition.

5 It is well known in the art that certain isolated replacements of amino acids, e.g., replacement of an amino acid residue with another related amino acid (i.e. isosteric and/or isoelectric mutations), can be carried out without major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded 10 amino acids are can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In similar 15 fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur -containing = cysteine and methionine. (see, for 20 example, *Biochemistry*, 2nd ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional *hedgehog* homolog (e.g. functional in the sense that it acts to mimic or antagonize the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or 25 competitively inhibit such a response. Polypeptides in which more than one replacement has taken place can readily be tested in the same manner.

It is specifically contemplated that the methods of the present invention can be carried using homologs of naturally occurring *hedgehog* proteins. In one embodiment, the invention contemplates using *hedgehog* polypeptides generated by combinatorial 30 mutagenesis. Such methods, as are known in the art, are convenient for generating both point and truncation mutants, and can be especially useful for identifying potential variant sequences (e.g. homologs) that are functional in binding to a receptor for *hedgehog* proteins. The purpose of screening such combinatorial libraries is to generate, for example, novel *hedgehog* homologs which can act as neuroprotective 35 agents. To illustrate, *hedgehog* homologs can be engineered by the present method to provide more efficient binding to a cognate receptor, such as *patched*, retaining

neuroprotective activity. Thus, combinatorially-derived homologs can be generated to have an increased potency relative to a naturally occurring form of the protein. Moreover, manipulation of certain domains of *hedgehog* by the present method can provide domains more suitable for use in fusion proteins, such as one that incorporates 5 portions of other proteins which are derived from the extracellular matrix and/or which bind extracellular matrix components.

To further illustrate the state of the art of combinatorial mutagenesis, it is noted that the review article of Gallop et al. (1994) *J Med Chem* 37:1233 describes the general state of the art of combinatorial libraries as of the earlier 1990's. In particular, 10 Gallop et al state at page 1239 "[s]creening the analog libraries aids in determining the minimum size of the active sequence and in identifying those residues critical for binding and intolerant of substitution". In addition, the Ladner et al. PCT publication WO90/02809, the Goeddel et al. U.S. Patent 5,223,408, and the Markland et al. PCT publication WO92/15679 illustrate specific techniques which one skilled in the art 15 could utilize to generate libraries of *hedgehog* variants which can be rapidly screened to identify variants/fragments which retained a particular activity of the *hedgehog* polypeptides. These techniques are exemplary of the art and demonstrate that large libraries of related variants/truncants can be generated and assayed to isolate particular variants without undue experimentation. Gustin et al. (1993) *Virology* 193:653, and 20 Bass et al. (1990) *Proteins: Structure, Function and Genetics* 8:309-314 also describe other exemplary techniques from the art which can be adapted as means for generating mutagenic variants of *hedgehog* polypeptides.

Indeed, it is plain from the combinatorial mutagenesis art that large scale mutagenesis of *hedgehog* proteins, without any preconceived ideas of which residues 25 were critical to the biological function, and generate wide arrays of variants having equivalent biological activity. Indeed, it is the ability of combinatorial techniques to screen billions of different variants by high throughout analysis that removes any requirement of *a priori* understanding or knowledge of critical residues.

To illustrate, the amino acid sequences for a population of *hedgehog* homologs 30 or other related proteins are aligned, preferably to promote the highest homology possible. Such a population of variants can include, for example, *hedgehog* homologs from one or more species. Amino acids which appear at each position of the aligned sequences are selected to create a degenerate set of combinatorial sequences. In a preferred embodiment, the variegated library of *hedgehog* variants is generated by 35 combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For instance, a mixture of synthetic oligonucleotides can be enzymatically

ligated into gene sequences such that the degenerate set of potential *hedgehog* sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g. for phage display) containing the set of *hedgehog* sequences therein.

5 As illustrated in PCT publication WO 95/18856, to analyze the sequences of a population of variants, the amino acid sequences of interest can be aligned relative to sequence homology. The presence or absence of amino acids from an aligned sequence of a particular variant is relative to a chosen consensus length of a reference sequence, which can be real or artificial.

10 In an illustrative embodiment, alignment of exons 1, 2 and a portion of exon 3 encoded sequences (e.g. the N-terminal approximately 221 residues of the mature protein) of each of the *Shh* clones produces a degenerate set of *Shh* polypeptides represented by the general formula:

15 C-G-P-G-R-G-X(1)-G-X(2)-R-R-H-P-K-K-L-T-P-L-A-Y-K-Q-F-I-P-N-
V-A-E-K-T-L-G-A-S-G-R-Y-E-G-K-I-X(3)-R-N-S-E-R-F-K-E-L-T-P-
N-Y-N-P-D-I-I-F-K-D-E-E-N-T-G-A-D-R-L-M-T-Q-R-C-K-D-K-L-N-
X(4)-L-A-I-S-V-M-N-X(5)-W-P-G-V-X(6)-L-R-V-T-E-G-W-D-E-D-G-
H-H-X(7)-E-E-S-L-H-Y-E-G-R-A-V-D-I-T-T-S-D-R-D-X(8)-S-K-Y-G-
X(9)-L-X(10)-R-L-A-V-E-A-G-F-D-W-V-Y-Y-E-S-K-A-H-I-H-C-S-V-
20 K-A-E-N-S-V-A-A-K-S-G-G-C-F-P-G-S-A-X(11)-V-X(12)-L-X(13)-
X(14)-G-G-X(15)-K-X(16)-V-K-D-L-X(17)-P-G-D-X(18)-V-L-A-A-
D-X(19)-X(20)-G-X(21)-L-X(22)-X(23)-S-D-F-X(24)-X(25)-F-X(26)-
D-R (SEQ ID No: 21),

25 wherein each of the degenerate positions "X" can be an amino acid which occurs in that position in one of the human, mouse, chicken or zebrafish *Shh* clones, or, to expand the library, each X can also be selected from amongst amino acid residue which would be conservative substitutions for the amino acids which appear naturally in each of those positions. For instance, Xaa(1) represents Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp ; Xaa(2) represents Arg, His or Lys; Xaa(3) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(4) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(5) represents Lys, Arg, His, Asn or Gln; Xaa(6) represents Lys, Arg or His; Xaa(7) represents Ser, Thr, Tyr, Trp or Phe; Xaa(8) represents Lys, Arg or His; Xaa(9) represents Met, Cys, Ser or Thr; Xaa(10) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(11) represents Leu, Val, Met, Thr or Ser; Xaa(12) represents His, Phe, Tyr, Ser, Thr, Met or Cys; Xaa(13) 30 represents Gln, Asn, Glu, or Asp; Xaa(14) represents His, Phe, Tyr, Thr, Gln, Asn, Glu
35

or Asp; Xaa(15) represents Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys; Xaa(16) represents Ala, Gly, Cys, Leu, Val or Met; Xaa(17) represents Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys; Xaa(18) represents Arg, Lys, Met or Ile; Xaa(19) represents Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met; Xaa(20) represents Ala, 5 Gly, Cys, Asp, Asn, Glu or Gln; Xaa(21) represents Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln; Xaa(22) represent Leu, Val, Met or Ile; Xaa(23) represents Phe, Tyr, Thr, His or Trp; Xaa(24) represents Ile, Val, Leu or Met; Xaa(25) represents Met, Cys, Ile, Leu, Val, Thr or Ser; Xaa(26) represents Leu, Val, Met, Thr or Ser. In an even more expansive library, each X can be selected from any amino acid.

10 In similar fashion, alignment of each of the human, mouse, chicken and zebrafish *hedgehog* clones, can provide a degenerate polypeptide sequence represented by the general formula:

C-G-P-G-R-G-X(1)-X(2)-X(3)-R-R-X(4)-X(5)-X(6)-P-K-X(7)-L-X(8)-
P-L-X(9)-Y-K-Q-F-X(10)-P-X(11)-X(12)-X(13)-E-X(14)-T-L-G-A-S-
15 G-X(15)-X(16)-E-G-X(17)-X(18)-X(19)-R-X(20)-S-E-R-F-X(21)-
X(22)-L-T-P-N-Y-N-P-D-I-I-F-K-D-E-E-N-X(23)-G-A-D-R-L-M-T-
X(24)-R-C-K-X(25)-X(26)-X(27)-N-X(28)-L-A-I-S-V-M-N-X(29)-W-
P-G-V-X(30)-L-R-V-T-E-G-X(31)-D-E-D-G-H-H-X(32)-X(33)-X(34)-
S-L-H-Y-E-G-R-A-X(35)-D-I-T-T-S-D-R-D-X(36)-X(37)-K-Y-G-
20 X(38)-L-X(39)-R-L-A-V-E-A-G-F-D-W-V-Y-Y-E-S-X(40)-X(41)-H-
X(42)-H-X(43)-S-V-K-X(44)-X(45) (SEQIDNo:22),

wherein, as above, each of the degenerate positions "X" can be an amino acid which occurs in a corresponding position in one of the wild-type clones, and may also include amino acid residue which would be conservative substitutions, or each X can be any 25 amino acid residue. In an exemplary embodiment, Xaa(1) represents Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr; Xaa(2) represents Gly, Ala, Val, Leu or Ile; Xaa(3) represents Gly, Ala, Val, Leu, Ile, Lys, His or Arg; Xaa(4) represents Lys, Arg or His; Xaa(5) represents Phe, Trp, Tyr or an amino acid gap; Xaa(6) represents Gly, Ala, Val, Leu, Ile or an amino acid gap; Xaa(7) represents Asn, Gln, His, Arg or Lys; Xaa(8) represents 30 Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(9) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(10) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(11) represents Ser, Thr, Gln or Asn; Xaa(12) represents Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(13) represents Gly, Ala, Val, Leu, Ile or Pro; Xaa(14) represents Arg, His or Lys; Xaa(15) represents Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys; Xaa(16) represents Gly, Ala, 35 Val, Leu, Ile, Phe or Tyr; Xaa(17) represents Arg, His or Lys; Xaa(18) represents Gly, Ala, Val, Leu, Ile, Ser or Thr; Xaa(19) represents Thr or Ser; Xaa(20) represents Gly,

Ala, Val, Leu, Ile, Asn or Gln; Xaa(21) represents Arg, His or Lys; Xaa(22) represents Asp or Glu; Xaa(23) represents Ser or Thr; Xaa(24) represents Glu, Asp, Gln or Asn; Xaa(25) represents Glu or Asp; Xaa(26) represents Arg, His or Lys; Xaa(27) represents Gly, Ala, Val, Leu or Ile; Xaa(28) represents Gly, Ala, Val, Leu, Ile, Thr or Ser; 5 Xaa(29) represents Met, Cys, Gln, Asn, Arg, Lys or His; Xaa(30) represents Arg, His or Lys; Xaa(31) represents Trp, Phe, Tyr, Arg, His or Lys; Xaa(32) represents Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe; Xaa(33) represents Gln, Asn, Asp or Glu; Xaa(34) represents Asp or Glu; Xaa(35) represents Gly, Ala, Val, Leu, or Ile; Xaa(36) represents Arg, His or Lys; Xaa(37) represents Asn, Gln, Thr or Ser; Xaa(38) represents Gly, Ala, 10 Val, Leu, Ile, Ser, Thr, Met or Cys; Xaa(39) represents Gly, Ala, Val, Leu, Ile, Thr or Ser; Xaa(40) represents Arg, His or Lys; Xaa(41) represents Asn, Gln, Gly, Ala, Val, Leu or Ile; Xaa(42) represents Gly, Ala, Val, Leu or Ile; Xaa(43) represents Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys; Xaa(44) represents Gly, Ala, Val, Leu, Ile, Thr or Ser; and Xaa(45) represents Asp or Glu.

15 There are many ways by which the library of potential *hedgehog* homologs can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the 20 desired set of potential *hedgehog* sequences. The synthesis of degenerate oligonucleotides is well known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton. Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. 25 (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

30 A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations, and for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of *hedgehog* homologs. The most widely used techniques for screening large gene 35 libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the

combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the illustrative assays described below are amenable to high through-put analysis as necessary to screen large numbers of degenerate *hedgehog* sequences 5 created by combinatorial mutagenesis techniques.

In one embodiment, the combinatorial library is designed to be secreted (e.g. the polypeptides of the library all include a signal sequence but no transmembrane or cytoplasmic domains), and is used to transfect a eukaryotic cell that can be co-cultured with neuronal cells. A functional *hedgehog* protein secreted by the cells expressing the 10 combinatorial library will diffuse to neighboring neuronal cells and induce a particular biological response, such as protection against cell death when treated with MPTP. The pattern of protection will resemble a gradient function, and will allow the isolation (generally after several repetitive rounds of selection) of cells producing *hedgehog* homologs active as neuroprotective agents with respect to the target neuronal cells

15 To illustrate, target neuronal cells are cultured in 24-well microtitre plates. Other eukaryotic cells are transfected with the combinatorial *hedgehog* gene library and cultured in cell culture inserts (e.g. Collaborative Biomedical Products, Catalog #40446) that are able to fit into the wells of the microtitre plate. The cell culture inserts are placed in the wells such that recombinant *hedgehog* homologs secreted by the cells 20 in the insert can diffuse through the porous bottom of the insert and contact the target cells in the microtitre plate wells. After a period of time sufficient for functional forms of a *hedgehog* protein to produce a measurable response in the target cells, such as neuroprotection, the inserts are removed and the effect of the variant *hedgehog* proteins on the target cells determined. Cells from the inserts corresponding to wells which 25 score positive for activity can be split and re-cultured on several inserts, the process being repeated until the active clones are identified.

In yet another screening assay, the candidate *hedgehog* gene products are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to associate with a *hedgehog*-binding moiety (such as the *patched* protein 30 or other *hedgehog* receptor) via this gene product is detected in a "panning assay". Such panning steps can be carried out on cells cultured from embryos. For instance, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 35 18:136-140). In a similar fashion, fluorescently labeled molecules which bind *hedgehog* can be used to score for potentially functional *hedgehog* homologs. Cells can

be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, separated by a fluorescence-activated cell sorter.

In an alternate embodiment, the gene library is expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign 5 peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at very high concentrations, large number of phage can be screened at one time. Second, since each infectious phage displays the combinatorial gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the 10 phage can be amplified by another round of infection. The group of almost identical *E.coli* filamentous phages M13, fd, and f1 are most often used in phage display libraries, as either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks 15 et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

In an illustrative embodiment, the recombinant phage antibody system (RPAS, Pharamacia Catalog number 27-9400-01) can be easily modified for use in expressing 20 and screening *hedgehog* combinatorial libraries. For instance, the pCANTAB 5 phagemid of the RPAS kit contains the gene which encodes the phage gIII coat protein. The *hedgehog* combinatorial gene library can be cloned into the phagemid adjacent to the gIII signal sequence such that it will be expressed as a gIII fusion protein. After ligation, the phagemid is used to transform competent *E. coli* TG1 cells. Transformed 25 cells are subsequently infected with M13KO7 helper phage to rescue the phagemid and its candidate *hedgehog* gene insert. The resulting recombinant phage contain phagemid DNA encoding a specific candidate *hedgehog*, and display one or more copies of the corresponding fusion coat protein. The phage-displayed candidate *hedgehog* proteins which are capable of binding an *hedgehog* receptor are selected or enriched by panning. 30 For instance, the phage library can be applied to cells which express the *patched* protein and unbound phage washed away from the cells. The bound phage is then isolated, and if the recombinant phage express at least one copy of the wild type gIII coat protein, they will retain their ability to infect *E. coli*. Thus, successive rounds of reinfection of *E. coli*, and panning will greatly enrich for *hedgehog* homologs, which can then be 35 screened for further biological activities in order to differentiate agonists and antagonists.

Combinatorial mutagenesis has a potential to generate very large libraries of mutant proteins, e.g., in the order of 10^{26} molecules. Combinatorial libraries of this size may be technically challenging to screen even with high throughput screening assays such as phage display. To overcome this problem, a new technique has been 5 developed recently, recursive ensemble mutagenesis (REM), which allows one to avoid the very high proportion of non-functional proteins in a random library and simply enhances the frequency of functional proteins, thus decreasing the complexity required to achieve a useful sampling of sequence space. REM is an algorithm which enhances the frequency of functional mutants in a library when an appropriate selection or 10 screening method is employed (Arkin and Yourvan, 1992, *PNAS USA* 89:7811-7815; Yourvan et al., 1992, *Parallel Problem Solving from Nature*, 2., In Maenner and Manderick, eds., Elsevier Publishing Co., Amsterdam, pp. 401-410; Delgrave et al., 1993, *Protein Engineering* 6(3):327-331).

The invention also provides for reduction of the *hedgehog* protein to generate 15 mimetics, e.g. peptide or non-peptide agents, which are able to mimic the neuroprotective activity of a naturally-occurring *hedgehog* polypeptide. Thus, such mutagenic techniques as described above are also useful to map the determinants of the *hedgehog* proteins which participate in protein-protein interactions involved in, for example, binding of the subject *hedgehog* polypeptide to other extracellular matrix 20 components such as its receptor(s). To illustrate, the critical residues of a subject *hedgehog* polypeptide which are involved in molecular recognition of an *hedgehog* receptor such as *patched* can be determined and used to generate *hedgehog*-derived peptidomimetics which competitively bind with that moiety. By employing, for example, scanning mutagenesis to map the amino acid residues of each of the subject 25 *hedgehog* proteins which are involved in binding other extracellular proteins, peptidomimetic compounds can be generated which mimic those residues of the *hedgehog* protein which facilitate the interaction. After distinguishing between agonist and antagonists, such agonistic mimetics may be used to mimic the normal function of a *hedgehog* protein as trophic for dopaminergic and GABA-nergic neurons. For 30 instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in 35 *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med*

Chem 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β -turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and β -aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and Dann et al. (1986) *Biochem Biophys Res Commun* 134:71).

Recombinantly produced forms of the *hedgehog* proteins can be produced using, e.g., expression vectors containing a nucleic acid encoding a *hedgehog* polypeptide, operably linked to at least one transcriptional regulatory sequence.

10 Operably linked is intended to mean that the nucleotide sequence is linked to a regulatory sequence in a manner which allows expression of the nucleotide sequence. Regulatory sequences are art-recognized and are selected to direct expression of a *hedgehog* polypeptide. Accordingly, the term transcriptional regulatory sequence includes promoters, enhancers and other expression control elements. Such regulatory sequences are described in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). For instance, any of a wide variety of expression control sequences, sequences that control the expression of a DNA sequence when operatively linked to it, may be used in these vectors to express DNA sequences encoding *hedgehog* polypeptide. Such useful expression control sequences, include, for example, a viral LTR, such as the LTR of the Moloney murine leukemia virus, the early and late promoters of SV40, adenovirus or cytomegalovirus immediate early promoter, the lac system, the trp system, the TAC or TRC system, T7 promoter whose expression is directed by T7 RNA polymerase, the major operator and promoter regions of phage λ , the control regions for fd coat protein, the promoter for 20 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase, e.g., Pho5, the promoters of the yeast α -mating factors, the polyhedron promoter of the baculovirus system and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof. It should be understood that the design of the expression vector 25 may depend on such factors as the choice of the host cell to be transformed and/or the type of protein desired to be expressed. Moreover, the vector's copy number, the ability to control that copy number and the expression of any other proteins encoded by the vector, such as antibiotic markers, should also be considered.

30 In addition to providing a ready source of *hedgehog* polypeptides for purification, the gene constructs of the present invention can also be used as a part of a gene therapy protocol to deliver nucleic acids encoding either a neuroprotective form of

a *hedgehog* polypeptide. Thus, another aspect of the invention features expression vectors for *in vivo* transfection of a *hedgehog* polypeptide in particular cell types so as cause ectopic expression of a *hedgehog* polypeptide in neuronal tissue.

Formulations of such expression constructs may be administered in any 5 biologically effective carrier, e.g. any formulation or composition capable of effectively delivering the recombinant gene to cells *in vivo*. Approaches include insertion of the *hedgehog* coding sequence in viral vectors including recombinant retroviruses, adenovirus, adeno-associated virus, and herpes simplex virus-1, or recombinant bacterial or eukaryotic plasmids. Viral vectors transfect cells directly; plasmid DNA 10 can be delivered with the help of, for example, cationic liposomes (lipofectin) or derivatized (e.g. antibody conjugated), polylysine conjugates, gramicidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or CaPO₄ precipitation carried out *in vivo*. It will be appreciated that because 15 transduction of appropriate target cells represents the critical first step in gene therapy, choice of the particular gene delivery system will depend on such factors as the phenotype of the intended target and the route of administration, e.g. locally or systemically. Furthermore, it will be recognized that the particular gene construct provided for *in vivo* transduction of *hedgehog* expression are also useful for *in vitro* transduction of cells, such as for use in the *ex vivo* tissue culture systems described 20 below.

A preferred approach for *in vivo* introduction of nucleic acid into a cell is by use of a viral vector containing nucleic acid, e.g. a cDNA, encoding the particular form of the *hedgehog* polypeptide desired. Infection of cells with a viral vector has the advantage that a large proportion of the targeted cells can receive the nucleic acid. 25 Additionally, molecules encoded within the viral vector, e.g., by a cDNA contained in the viral vector, are expressed efficiently in cells which have taken up viral vector nucleic acid.

Retrovirus vectors and adeno-associated virus vectors are generally understood 30 to be the recombinant gene delivery system of choice for the transfer of exogenous genes *in vivo*, particularly into humans. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated into the chromosomal DNA of the host. A major prerequisite for the use of retroviruses is to ensure the safety of their use, particularly with regard to the possibility of the spread of wild-type virus in the cell population. The development of specialized cell lines 35 (termed "packaging cells") which produce only replication-defective retroviruses has increased the utility of retroviruses for gene therapy, and defective retroviruses are well

characterized for use in gene transfer for gene therapy purposes (for a review see Miller, A.D. (1990) *Blood* 76:271). Thus, recombinant retrovirus can be constructed in which part of the retroviral coding sequence (*gag*, *pol*, *env*) has been replaced by nucleic acid encoding a *hedgehog* polypeptide and renders the retrovirus replication 5 defective. The replication defective retrovirus is then packaged into virions which can be used to infect a target cell through the use of a helper virus by standard techniques. Protocols for producing recombinant retroviruses and for infecting cells *in vitro* or *in vivo* with such viruses can be found in Current Protocols in Molecular Biology, Ausubel, F.M. et al. (eds.) Greene Publishing Associates, (1989), Sections 9.10-9.14 10 and other standard laboratory manuals. Examples of suitable retroviruses include pLJ, pZIP, pWE and pEM which are well known to those skilled in the art. Examples of suitable packaging virus lines for preparing both ecotropic and amphotropic retroviral systems include Crip, Cre, 2 and Am. Retroviruses have been used to introduce a variety of genes into many different cell types, including neuronal cells, *in vitro* and/or 15 *in vivo* (see for example Eglitis, et al. (1985) *Science* 230:1395-1398; Danos and Mulligan (1988) *Proc. Natl. Acad. Sci. USA* 85:6460-6464; Wilson et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:3014-3018; Armentano et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:6141-6145; Huber et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:8039-8043; Ferry et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:8377-8381; Chowdhury et al. (1991) 20 *Science* 254:1802-1805; van Beusechem et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:7640-7644; Kay et al. (1992) *Human Gene Therapy* 3:641-647; Dai et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:10892-10895; Hwu et al. (1993) *J. Immunol.* 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO 89/02468; PCT Application WO 89/05345; and PCT 25 Application WO 92/07573).

Furthermore, it has been shown that it is possible to limit the infection spectrum of retroviruses and consequently of retroviral-based vectors, by modifying the viral packaging proteins on the surface of the viral particle (see, for example PCT publications WO93/25234 and WO94/06920). For instance, strategies for the 30 modification of the infection spectrum of retroviral vectors include: coupling antibodies specific for cell surface antigens to the viral *env* protein (Roux et al. (1989) *PNAS* 86:9079-9083; Julian et al. (1992) *J. Gen Virol* 73:3251-3255; and Goud et al. (1983) *Virology* 163:251-254); or coupling cell surface receptor ligands to the viral *env* proteins (Neda et al. (1991) *J Biol Chem* 266:14143-14146). Coupling can be in the 35 form of the chemical cross-linking with a protein or other variety (e.g. lactose to convert the *env* protein to an asialoglycoprotein), as well as by generating fusion

proteins (e.g. single-chain antibody/*env* fusion proteins). This technique, while useful to limit or otherwise direct the infection to certain tissue types, can also be used to convert an ecotropic vector in to an amphotropic vector.

Moreover, use of retroviral gene delivery can be further enhanced by the use of 5 tissue- or cell-specific transcriptional regulatory sequences which control expression of the *hedgehog* gene of the retroviral vector.

Another viral gene delivery system useful in the present method utilizes 10 adenovirus-derived vectors. The genome of an adenovirus can be manipulated such that it encodes and expresses a gene product of interest but is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. See for example Berkner et al. (1988) *BioTechniques* 6:616; Rosenfeld et al. (1991) *Science* 252:431-434; and 15 Rosenfeld et al. (1992) *Cell* 68:143-155. Suitable adenoviral vectors derived from the adenovirus strain Ad type 5 dl324 or other strains of adenovirus (e.g., Ad2, Ad3, Ad7 etc.) are well known to those skilled in the art. Recombinant adenoviruses can be 15 advantageous in certain circumstances in that they can be used to infect a wide variety of cell types, including neuronal cells (Rosenfeld et al. (1992) cited *supra*).

Furthermore, the virus particle is relatively stable and amenable to purification 20 and concentration, and as above, can be modified so as to affect the spectrum of infectivity. Additionally, introduced adenoviral DNA (and foreign DNA contained therein) is not integrated into the genome of a host cell but remains episomal, thereby avoiding potential problems that can occur as a result of insertional mutagenesis in situations where introduced DNA becomes integrated into the host genome (e.g., retroviral DNA). Moreover, the carrying capacity of the adenoviral genome for foreign 25 DNA is large (up to 8 kilobases) relative to other gene delivery vectors (Berkner et al. cited *supra*; Haj-Ahmand and Graham (1986) *J. Virol.* 57:267). Most replication-defective adenoviral vectors currently in use and therefore favored by the present invention are deleted for all or parts of the viral E1 and E3 genes but retain as much as 30 80% of the adenoviral genetic material (see, e.g., Jones et al. (1979) *Cell* 16:683; Berkner et al., *supra*; and Graham et al. in Methods in Molecular Biology, E.J. Murray, Ed. (Humana, Clifton, NJ, 1991) vol. 7. pp. 109-127). Expression of the inserted *hedgehog* gene can be under control of, for example, the E1A promoter, the major late promoter (MLP) and associated leader sequences, the E3 promoter, or exogenously added promoter sequences.

In addition to viral transfer methods, such as those illustrated above, non-viral 35 methods can also be employed to cause expression of a *hedgehog* polypeptide in the

tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral gene delivery systems of the present invention rely on endocytic pathways for the uptake of the *hedgehog* 5 polypeptide gene by the targeted cell. Exemplary gene delivery systems of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

In clinical settings, the gene delivery systems for the therapeutic *hedgehog* gene can be introduced into a patient by any of a number of methods, each of which is 10 familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g. by intravenous injection, and specific transduction of the protein in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor 15 gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the animal being quite localized. For example, the gene delivery vehicle can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g. Chen et al. (1994) *PNAS* 91: 20 3054-3057). A *hedgehog* expression construct can be delivered in a gene therapy construct to dermal cells by, e.g., electroporation using techniques described, for example, by Dev et al. ((1994) *Cancer Treat Rev* 20:105-115).

The pharmaceutical preparation of the gene therapy construct can consist 25 essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g. retroviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system.

In yet another embodiment, the *hedgehog* or ptc therapeutic can be a "gene activation" construct which, by homologous recombination with a genomic DNA, alters 30 the transcriptional regulatory sequences of an endogenous gene. For instance, the gene activation construct can replace the endogenous promoter of a *hedgehog* gene with a heterologous promoter, e.g., one which causes constitutive expression of the *hedgehog* gene or which causes inducible expression of the gene under conditions different from the normal expression pattern of the gene. Other genes in the *patched* signaling pathway 35 can be similarly targeted. A variety of different formats for the gene activation constructs are available. See, for example, the Transkaryotic Therapies, Inc PCT

publications WO93/09222, WO95/31560, WO96/29411, WO95/31560 and WO94/12650.

In preferred embodiments, the nucleotide sequence used as the gene activation construct can be comprised of (1) DNA from some portion of the endogenous *hedgehog* gene (exon sequence, intron sequence, promoter sequences, etc.) which direct recombination and (2) heterologous transcriptional regulatory sequence(s) which is to be operably linked to the coding sequence for the genomic *hedgehog* gene upon recombination of the gene activation construct. For use in generating cultures of *hedgehog* producing cells, the construct may further include a reporter gene to detect 10 the presence of the knockout construct in the cell.

The gene activation construct is inserted into a cell, and integrates with the genomic DNA of the cell in such a position so as to provide the heterologous regulatory sequences in operative association with the native *hedgehog* gene. Such insertion occurs by homologous recombination, i.e., recombination regions of the activation 15 construct that are homologous to the endogenous *hedgehog* gene sequence hybridize to the genomic DNA and recombine with the genomic sequences so that the construct is incorporated into the corresponding position of the genomic DNA.

The terms "recombination region" or "targeting sequence" refer to a segment (i.e., a portion) of a gene activation construct having a sequence that is substantially 20 identical to or substantially complementary to a genomic gene sequence, e.g., including 5' flanking sequences of the genomic gene, and can facilitate homologous recombination between the genomic sequence and the targeting transgene construct.

As used herein, the term "replacement region" refers to a portion of a activation 25 construct which becomes integrated into an endogenous chromosomal location following homologous recombination between a recombination region and a genomic sequence.

The heterologous regulatory sequences, e.g., which are provided in the replacement region, can include one or more of a variety elements, including: 30 promoters (such as constitutive or inducible promoters), enhancers, negative regulatory elements, locus control regions, transcription factor binding sites, or combinations thereof. Promoters/enhancers which may be used to control the expression of the targeted gene *in vivo* include, but are not limited to, the cytomegalovirus (CMV) promoter/enhancer (Karasuyama et al., 1989, *J. Exp. Med.*, 169:13), the human β -actin promoter (Gunning et al. (1987) *PNAS* 84:4831-4835), the glucocorticoid-inducible promoter present in the mouse mammary tumor virus long terminal repeat (MMTV 35

LTR) (Klessig et al. (1984) *Mol. Cell Biol.* 4:1354-1362), the long terminal repeat sequences of Moloney murine leukemia virus (MuLV LTR) (Weiss et al. (1985) *RNA Tumor Viruses*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York), the SV40 early or late region promoter (Bernoist et al. (1981) *Nature* 290:304-310; 5 Templeton et al. (1984) *Mol. Cell Biol.*, 4:817; and Sprague et al. (1983) *J. Virol.*, 45:773), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (RSV) (Yamamoto et al., 1980, *Cell*, 22:787-797), the herpes simplex virus (HSV) thymidine kinase promoter/enhancer (Wagner et al. (1981) *PNAS* 82:3567-71), and the herpes simplex virus LAT promoter (Wolfe et al. (1992) *Nature Genetics*, 1:379-384).

10 In an exemplary embodiment, portions of the 5' flanking region of the human Shh gene are amplified using primers which add restriction sites, to generate the following fragments

5' -gcgcgcgttcgaaGCGAGGCAGCCAGCGAGGGAGAGAGCGAGCGGGCGAGCCGGA-
GCGAGGAAatcgatgcgcgc (primer 1)

15

5' -gcgcgcagatctGGGAAAGCGCAAGAGAGAGCGCACACGCACACACCCGCCGCG-
CGCACTCGggatccgcgcgc (primer 2)

20 As illustrated, primer 1 includes a 5' non-coding region of the human Shh gene and is flanked by an AsuII and Clal restriction sites. Primer 2 includes a portion of the 5' non-coding region immediately 3' to that present in primer 1. The hedgehog gene sequence is flanked by XhoII and BamHI restriction sites. The purified amplimers are cut with each of the enzymes as appropriate.

25 The vector pCDNA1.1 (Invitrogen) includes a CMV promoter. The plasmid is cut with with AsuII, which cleaves just 3' to the CMV promoter sequence. The AsuII/Clal fragment of primer 1 is ligated to the AsuII cleavage site of the pcDNA vector. The Clal/AsuII ligation destroys the AsuII site at the 3' end of a properly inserted primer 1.

30 The vector is then cut with BamHI, and an XhoII/BamHI fragment of primer 2 is ligated to the BamHI cleavage site. As above, the BamHI/XhoII ligation destroys the BamHI site at the 5' end of a properly inserted primer 2.

Individual colonies are selected, cut with AsuII and BamHI, and the size of the AsuII/BamHI fragment determined. Colonies in which both the primer 1 and primer 2

sequences are correctly inserted are further amplified, an cut with *Asu*II and *Bam*HI to produce the gene activation construct

5 cgaaggcgaggcaggcagcgaggagagagcgagcggcgagccggcgaggaaATCG
AAGGTTCGAATCCTCCCCACCACCATCACTTCAAAAGTCCGAAAGAATCTGCTCC
CTGCTTGTGTGGAGGTGCGCTGAGTAGTGCAGTAAATTAAGCTACAACAAG
GCAAGGCTTGACCGACAATTGCATGAAGAATCTGCTTAGGGTTAGGCCTTGCCTG
CTTCGCGATGTACGGGCCAGATATACGCCTGACATTGATTATTGACTAGTTATTAAT
AGTAATCAATTACGGGGTCATTAGTCATAGCCCATAATGGAGTCCCGCTTACATA
ACTTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCA
10 ATAATGACGTATGTTCCCATACTAACGCCAATAGGGACTTCCATTGACGTCAATGGG
TGGACTATTTACGGTAAACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAG
TACGCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTAC
ATGACCTTATGGACTTCCACTTGGCAGTACATCTACGTATTAGTCATCGCTATTA
CCATGGTGATGCGGTTTGGCAGTACATCAATGGCGTGGATAGCGGTTGACTCAGC
15 GGGATTCCAAGTCTCCACCCATTGACGTCAATGGAGTTGGCATTGGCACCAAAAT
CAACGGGACTTCCAAAATGTCGTAACAACCTCCGCCATTGACGCAAATGGCGGTA
GGCGTGTACGGTGGAGGTCTATATAAGCAGAGCTCTGGCTAACTAGAGAACCCAC
TGCTTACTGGCTATCGAAATTAAATACGACTCACTATAGGGAGACCAAGCTGGTAC
CGAGCTCGGATCgatctggaaagcgcaagagagagcgcacacgcacacacccgcccgc
20 gcgcactcgg

25 In this construct, the flanking primer 1 and primer 2 sequences provide the recombination region which permits the insertion of the CMV promoter in front of the coding sequence for the human *Shh* gene. Other heterologous promoters (or other transcriptional regulatory sequences) can be inserted in a genomic *hedgehog* gene by a similar method.

In still other embodiments, the replacement region merely deletes a negative transcriptional control element of the native gene, e.g., to activate expression, or ablates a positive control element, e.g., to inhibit expression of the targeted gene.

30 V. EXEMPLARY PTC THERAPEUTIC COMPOUNDS.

35 In another embodiment, the subject method is carried out using a ptc therapeutic composition. Such compositions can be generated with, for example, compounds which bind to patched and alter its signal transduction activity, compounds which alter the binding and/or enzymatic activity of a protein (e.g., intracellular) involved in patched signal pathway, and compounds which alter the level of expression of a

hedgehog protein, a patched protein or a protein involved in the intracellular signal transduction pathway of *patched*.

The availability of purified and recombinant *hedgehog* polypeptides facilitates the generation of assay systems which can be used to screen for drugs, such as small organic molecules, which are either agonists or antagonists of the normal cellular function of a *hedgehog* and/or *patched* protein, particularly in their role in the pathogenesis of neuronal cell death. In one embodiment, the assay evaluates the ability of a compound to modulate binding between a *hedgehog* polypeptide and a *hedgehog* receptor such as *patched*. In other embodiments, the assay merely scores for the ability 5 of a test compound to alter the signal transduction activity of the *patched* protein. In this manner, a variety of *hedgehog* and/or *ptc* therapeutics, which will include ones with neuroprotective activity, can be identified. A variety of assay formats will suffice 10 and, in light of the present disclosure, will be comprehended by skilled artisan.

In many drug screening programs which test libraries of compounds and natural 15 extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is 20 mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with receptor proteins.

Accordingly, in an exemplary screening assay for *ptc* therapeutics, the 25 compound of interest is contacted with a mixture including a *hedgehog* receptor protein (e.g., a cell expressing the *patched* receptor) and a *hedgehog* protein under conditions in which it is ordinarily capable of binding the *hedgehog* protein. To the mixture is then added a composition containing a test compound. Detection and quantification of receptor/*hedgehog* complexes provides a means for determining the test compound's 30 efficacy at inhibiting (or potentiating) complex formation between the receptor protein and the *hedgehog* polypeptide. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified *hedgehog* polypeptide is added to the receptor protein, and the formation of receptor/*hedgehog* complex is quantitated in the absence of the test compound.

In other embodiments, a ptc therapeutic of the present invention is one which disrupts the association of *patched* with *smoothened*.

Agonist and antagonists of neuroprotection can be distinguished, and the efficacy of the compound can be assessed, by subsequent testing with neuronal cells.

5 In an illustrative embodiment, the polypeptide utilized as a *hedgehog* receptor can be generated from the *patched* protein. Accordingly, an exemplary screening assay includes all or a suitable portion of the *patched* protein which can be obtained from, for example, the human *patched* gene (GenBank U43148) or other vertebrate sources (see GenBank Accession numbers U40074 for chicken *patched* and U46155 for mouse 10 *patched*), as well as from drosophila (GenBank Accession number M28999) or other invertebrate sources. The *patched* protein can be provided in the screening assay as a whole protein (preferably expressed on the surface of a cell), or alternatively as a fragment of the full length protein which binds to *hedgehog* polypeptides, e.g., as one or both of the substantial extracellular domains (e.g. corresponding to residues Asn120- 15 Ser438 and/or Arg770-Trp1027 of the human *patched* protein). For instance, the *patched* protein can be provided in soluble form, as for example a preparation of one of the extracellular domains, or a preparation of both of the extracellular domains which are covalently connected by an unstructured linker (see, for example, Huston et al. (1988) PNAS 85:4879; and U.S. Patent No. 5,091,513). In other embodiments, the 20 protein can be provided as part of a liposomal preparation or expressed on the surface of a cell. The *patched* protein can be derived from a recombinant gene, e.g., being ectopically expressed in a heterologous cell. For instance, the protein can be expressed on oocytes, mammalian cells (e.g., COS, CHO, 3T3 or the like), or yeast cell by standard recombinant DNA techniques. These recombinant cells can be used for 25 receptor binding, signal transduction or gene expression assays. Marigo et al. (1996) *Development* 122:1225-1233 illustrates a binding assay of human *hedgehog* to chick *patched* protein ectopically expressed in *Xenopus laevis* oocytes. The assay system of Marigo et al. can be adapted to the present drug screening assays. As illustrated in that reference, *Shh* binds to the *patched* protein in a selective, saturable, dose-dependent 30 manner, thus demonstrating that *patched* is a receptor for *Shh*.

Complex formation between the *hedgehog* polypeptide and a *hedgehog* receptor may be detected by a variety of techniques. For instance, modulation of the formation of complexes can be quantitated using, for example, detectably labelled proteins such as radiolabelled, fluorescently labelled, or enzymatically labelled *hedgehog* 35 polypeptides, by immunoassay, or by chromatographic detection.

Typically, for cell-free assays, it will be desirable to immobilize either the *hedgehog* receptor or the *hedgehog* polypeptide to facilitate separation of receptor/*hedgehog* complexes from uncomplexed forms of one of the proteins, as well as to accommodate automation of the assay. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase/receptor (GST/receptor) fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the *hedgehog* polypeptide, e.g. an ³⁵S-labeled *hedgehog* polypeptide, and the test compound and incubated under conditions conducive to complex formation, e.g. at physiological conditions for salt and pH, though slightly more stringent conditions may be desired. Following incubation, the beads are washed to remove any unbound *hedgehog* polypeptide, and the matrix bead-bound radiolabel determined directly (e.g. beads placed in scintillant), or in the supernatant after the receptor/*hedgehog* complexes are dissociated. Alternatively, the complexes can be dissociated from the bead, separated by SDS-PAGE gel, and the level of *hedgehog* polypeptide found in the bead fraction quantitated from the gel using standard electrophoretic techniques.

Other techniques for immobilizing proteins on matrices are also available for use in the subject assay. For instance, soluble portions of the *hedgehog* receptor protein can be immobilized utilizing conjugation of biotin and streptavidin. For instance, biotinylated receptor molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with the *hedgehog* receptor but which do not interfere with *hedgehog* binding can be derivatized to the wells of the plate, and the receptor trapped in the wells by antibody conjugation. As above, preparations of a *hedgehog* polypeptide and a test compound are incubated in the receptor-presenting wells of the plate, and the amount of receptor/*hedgehog* complex trapped in the well can be quantitated. Exemplary methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the *hedgehog* polypeptide, or which are reactive with the receptor protein and compete for binding with the *hedgehog* polypeptide; as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the *hedgehog* polypeptide. In the instance of the latter, the enzyme can be chemically conjugated or provided as a fusion protein with the *hedgehog* polypeptide. To illustrate, the *hedgehog* polypeptide can be

chemically cross-linked or genetically fused with alkaline phosphatase, and the amount of *hedgehog* polypeptide trapped in the complex can be assessed with a chromogenic substrate of the enzyme, e.g. paranitrophenylphosphate. Likewise, a fusion protein comprising the *hedgehog* polypeptide and glutathione-S-transferase can be provided, 5 and complex formation quantitated by detecting the GST activity using 1-chloro-2,4-dinitrobenzene (Habig et al (1974) *J Biol Chem* 249:7130).

For processes which rely on immunodetection for quantitating one of the proteins trapped in the complex, antibodies against the protein, such as the anti-*hedgehog* antibodies described herein, can be used. Alternatively, the protein to be 10 detected in the complex can be "epitope tagged" in the form of a fusion protein which includes, in addition to the *hedgehog* polypeptide or *hedgehog* receptor sequence, a second polypeptide for which antibodies are readily available (e.g. from commercial sources). For instance, the GST fusion proteins described above can also be used for quantification of binding using antibodies against the GST moiety. Other useful 15 epitope tags include myc-epitopes (e.g., see Ellison et al. (1991) *J Biol Chem* 266:21150-21157) which includes a 10-residue sequence from c-myc, as well as the pFLAG system (International Biotechnologies, Inc.) or the pEZZ-protein A system (Pharamacia, NJ).

Where the desired portion of the *hedgehog* receptor (or other *hedgehog* binding 20 molecule) cannot be provided in soluble form, liposomal vesicles can be used to provide manipulatable and isolatable sources of the receptor. For example, both authentic and recombinant forms of the *patched* protein can be reconstituted in artificial lipid vesicles (e.g. phosphatidylcholine liposomes) or in cell membrane-derived vesicles (see, for example, Bear et al. (1992) *Cell* 68:809-818; Newton et al. (1983) 25 *Biochemistry* 22:6110-6117; and Reber et al. (1987) *J Biol Chem* 262:11369-11374).

In addition to cell-free assays, such as described above, the readily available source of *hedgehog* proteins provided by the art also facilitates the generation of cell-based assays for identifying small molecule agonists of the neuroprotective activity of wild-type *hedgehog* proteins. Analogous to the cell-based assays described above for 30 screening combinatorial libraries, neuronal cells which are sensitive to *hedgehog*-dependent protection, such as dopaminergic and GABA-nergic neurons, can be contacted with a *hedgehog* protein and a test agent of interest, with the assay scoring for anything from simple binding to the cell to trophic responses by the target cell in the presence and absence of the test agent. As with the cell-free assays, agents which 35 produce a statistically significant change in *hedgehog* activities (either inhibition or potentiation) can be identified.

In other embodiments, the cell-based assay scores for agents which disrupt association of *patched* and *smoothened* proteins, e.g., in the cell surface membrane or liposomal preparation.

5 In addition to characterizing cells that naturally express the *patched* protein, cells which have been genetically engineered to ectopically express *patched* can be utilized for drug screening assays. As an example, cells which either express low levels or lack expression of the *patched* protein, e.g. *Xenopus laevis* oocytes, COS cells or yeast cells, can be genetically modified using standard techniques to ectopically express the *patched* protein. (see Marigo et al., *supra*).

10 The resulting recombinant cells, e.g., which express a functional *patched* receptor, can be utilized in receptor binding assays to identify agonist or antagonists of *hedgehog* binding. Binding assays can be performed using whole cells. Furthermore, the recombinant cells of the present invention can be engineered to include other heterologous genes encoding proteins involved in *hedgehog*-dependent signal pathways.

15 For example, the gene products of one or more of *smoothened*, *costal-2* and/or *fused* can be co-expressed with *patched* in the reagent cell, with assays being sensitive to the functional reconstitution of the *hedgehog* signal transduction cascade.

20 Alternatively, liposomal preparations using reconstituted *patched* protein can be utilized. *Patched* protein purified from detergent extracts from both authentic and recombinant origins can be reconstituted in artificial lipid vesicles (e.g. phosphatidylcholine liposomes) or in cell membrane-derived vesicles (see, for example, Bear et al. (1992) *Cell* 68:809-818; Newton et al. (1983) *Biochemistry* 22:6110-6117; and Reber et al. (1987) *J Biol Chem* 262:11369-11374). The lamellar structure and size of the resulting liposomes can be characterized using electron microscopy. External 25 orientation of the *patched* protein in the reconstituted membranes can be demonstrated, for example, by immunoelectron microscopy. The *hedgehog* protein binding activity of liposomes containing *patched* and liposomes without the protein in the presence of candidate agents can be compared in order to identify potential modulators of the *hedgehog-patched* interaction.

30 The *hedgehog* protein used in these cell-based assays can be provided as a purified source (natural or recombinant in origin), or in the form of cells/tissue which express the protein and which are co-cultured with the target cells. As in the cell-free assays, where simple binding (rather than induction) is the *hedgehog* activity scored for in the assay, the protein can be labelled by any of the above-mentioned techniques, e.g., 35 fluorescently, enzymatically or radioactively, or detected by immunoassay.

In addition to binding studies, functional assays can be used to identify modulators, i.e., agonists of *hedgehog* or *patched* activities. By detecting changes in intracellular signals, such as alterations in second messengers or gene expression in *patched*-expressing cells contacted with a test agent, candidate antagonists to *patched* 5 signaling can be identified (e.g., having a *hedgehog*-like activity).

A number of gene products have been implicated in *patched*-mediated signal transduction, including *patched*, the transcription factor *cubitus interruptus* (ci), the serine/threonine kinase *fused* (fu) and the gene products of *costal-2*, *smoothened* and *suppressor of fused*.

10 The interaction of a *hedgehog* protein with *patched* sets in motion a cascade involving the activation and inhibition of downstream effectors, the ultimate consequence of which is, in some instances, a detectable change in the transcription or translation of a gene. Potential transcriptional targets of *patched* signaling are the *patched* gene itself (Hidalgo and Ingham, 1990 *Development* 110, 291-301; Marigo et 15 al., 1996) and the vertebrate homologs of the *drosophila cubitus interruptus* gene, the *GLI* genes (Hui et al. (1994) *Dev Biol* 162:402-413). *Patched* gene expression has been shown to be induced in cells of the limb bud and the neural plate that are responsive to *Shh*. (Marigo et al. (1996) *PNAS*, in press; Marigo et al. (1996) *Development* 122:1225-1233). The *GLI* genes encode putative transcription factors having zinc finger DNA 20 binding domains (Orenic et al. (1990) *Genes & Dev* 4:1053-1067; Kinzler et al. (1990) *Mol Cell Biol* 10:634-642). Transcription of the *GLI* gene has been reported to be upregulated in response to *hedgehog* in limb buds, while transcription of the *GLI3* gene is downregulated in response to *hedgehog* induction (Marigo et al. (1996) *Development* 122:1225-1233). By selecting transcriptional regulatory sequences from 25 such target genes, e.g. from *patched* or *GLI* genes, that are responsible for the up- or down regulation of these genes in response to *patched* signalling, and operatively linking such promoters to a reporter gene, one can derive a transcription based assay which is sensitive to the ability of a specific test compound to modify *patched* signalling pathways. Expression of the reporter gene, thus, provides a valuable 30 screening tool for the development of compounds that act as antagonists of *ptc*, e.g., which may be useful as neuroprotective agents.

35 Reporter gene based assays of this invention measure the end stage of the above described cascade of events, e.g., transcriptional modulation. Accordingly, in practicing one embodiment of the assay, a reporter gene construct is inserted into the reagent cell in order to generate a detection signal dependent on *ptc* signaling. To identify potential regulatory elements responsive to *ptc* signaling present in the

transcriptional regulatory sequence of a target gene, nested deletions of genomic clones of the target gene can be constructed using standard techniques. See, for example, Current Protocols in Molecular Biology, Ausubel, F.M. et al. (eds.) Greene Publishing Associates, (1989); U.S. Patent 5,266,488; Sato et al. (1995) *J Biol Chem* 270:10314-5 10322; and Kube et al. (1995) *Cytokine* 7:1-7. A nested set of DNA fragments from the gene's 5'-flanking region are placed upstream of a reporter gene, such as the luciferase gene, and assayed for their ability to direct reporter gene expression in *patched* expressing cells. Host cells transiently transfected with reporter gene constructs can be scored for the induction of expression of the reporter gene in the presence and absence 10 of *hedgehog* to determine regulatory sequences which are responsive to *patched*-dependent signalling.

In practicing one embodiment of the assay, a reporter gene construct is inserted into the reagent cell in order to generate a detection signal dependent on second messengers generated by induction with *hedgehog* protein. Typically, the reporter gene 15 construct will include a reporter gene in operative linkage with one or more transcriptional regulatory elements responsive to the *hedgehog* activity, with the level of expression of the reporter gene providing the *hedgehog*-dependent detection signal. The amount of transcription from the reporter gene may be measured using any method known to those of skill in the art to be suitable. For example, mRNA expression from 20 the reporter gene may be detected using RNase protection or RNA-based PCR, or the protein product of the reporter gene may be identified by a characteristic stain or an intrinsic activity. The amount of expression from the reporter gene is then compared to the amount of expression in either the same cell in the absence of the test compound (or *hedgehog*) or it may be compared with the amount of transcription in a substantially 25 identical cell that lacks the target receptor protein. Any statistically or otherwise significant difference in the amount of transcription indicates that the test compound has in some manner altered the signal transduction of the *patched* protein, e.g., the test compound is a potential ptc therapeutic.

As described in further detail below, in preferred embodiments the gene product 30 of the reporter is detected by an intrinsic activity associated with that product. For instance, the reporter gene may encode a gene product that, by enzymatic activity, gives rise to a detection signal based on color, fluorescence, or luminescence. In other preferred embodiments, the reporter or marker gene provides a selective growth advantage, e.g., the reporter gene may enhance cell viability, relieve a cell nutritional 35 requirement, and/or provide resistance to a drug.

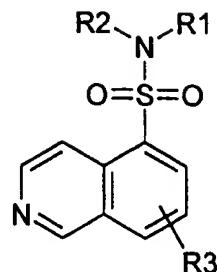
Preferred reporter genes are those that are readily detectable. The reporter gene may also be included in the construct in the form of a fusion gene with a gene that includes desired transcriptional regulatory sequences or exhibits other desirable properties. Examples of reporter genes include, but are not limited to CAT 5 (chloramphenicol acetyl transferase) (Alton and Vapnek (1979), *Nature* 282: 864-869) luciferase, and other enzyme detection systems, such as beta-galactosidase; firefly luciferase (deWet et al. (1987), *Mol. Cell. Biol.* 7:725-737); bacterial luciferase (Engebrecht and Silverman (1984), *PNAS* 1: 4154-4158; Baldwin et al. (1984), *Biochemistry* 23: 3663-3667); alkaline phosphatase (Toh et al. (1989) *Eur. J. Biochem.* 10 182: 231-238, Hall et al. (1983) *J. Mol. Appl. Gen.* 2: 101), human placental secreted alkaline phosphatase (Cullen and Malim (1992) *Methods in Enzymol.* 216:362-368).

Transcriptional control elements which may be included in a reporter gene construct include, but are not limited to, promoters, enhancers, and repressor and activator binding sites. Suitable transcriptional regulatory elements may be derived 15 from the transcriptional regulatory regions of genes whose expression is induced after modulation of a *patched* signal transduction pathway. The characteristics of preferred genes from which the transcriptional control elements are derived include, but are not limited to, low or undetectable expression in quiescent cells, rapid induction at the transcriptional level within minutes of extracellular stimulation, induction that is 20 transient and independent of new protein synthesis, subsequent shut-off of transcription requires new protein synthesis, and mRNAs transcribed from these genes have a short half-life. It is not necessary for all of these properties to be present.

In yet other embodiments, second messenger generation can be measured directly in the detection step, such as mobilization of intracellular calcium, 25 phospholipid metabolism or adenylate cyclase activity are quantitated, for instance, the products of phospholipid hydrolysis IP₃, DAG or cAMP could be measured. For example, recent studies have implicated protein kinase A (PKA) as a possible component of *hedgehog/patched* signaling (Hammerschmidt et al. (1996) *Genes & Dev* 10:647). High PKA activity has been shown to antagonize *hedgehog* signaling in these 30 systems. Conversely, inhibitors of PKA will mimic and/or potentiate the action of *hedgehog*. Although it is unclear whether PKA acts directly downstream or in parallel with *hedgehog* signaling, it is possible that *hedgehog* signalling occurs via inhibition of PKA activity. Thus, detection of PKA activity provides a potential readout for the instant assays.

35 In a preferred embodiment, the *ptc* therapeutic is a PKA inhibitor. A variety of PKA inhibitors are known in the art, including both peptidyl and organic compounds.

For instance, the *ptc* therapeutic can be a 5-isoquinolinesulfonamide, such as represented in the general formula:



5 wherein,

10 R_1 and R_2 each can independently represent hydrogen, and as valence and stability permit a lower alkyl, a lower alkenyl, a lower alkynyl, a carbonyl (such as a carboxyl, an ester, a formate, or a ketone), a thiocarbonyl (such as a thioester, a thioacetate, or a thioformate), an amino, an acylamino, an amido, a cyano, a nitro, an azido, a sulfate, a sulfonate, a sulfonamido, $-(CH_2)_m-R_8$, $-(CH_2)_m-OH$, $-(CH_2)_m-O-$ lower alkyl, $-(CH_2)_m-O$ -lower alkenyl, $-(CH_2)_n-O-(CH_2)_m-R_8$, $-(CH_2)_m-SH$, $-(CH_2)_m-S$ -lower alkyl, $-(CH_2)_m-S$ -lower alkenyl, $-(CH_2)_n-S-(CH_2)_m-R_8$, or

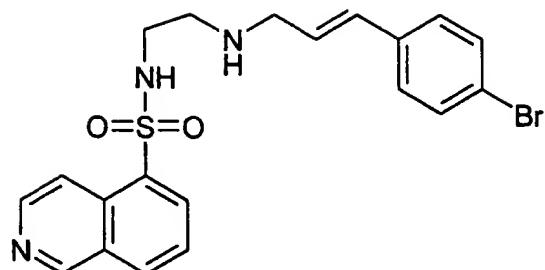
15 R_1 and R_2 taken together with N form a heterocycle (substituted or unsubstituted);

20 R_3 is absent or represents one or more substitutions to the isoquinoline ring such as a lower alkyl, a lower alkenyl, a lower alkynyl, a carbonyl (such as a carboxyl, an ester, a formate, or a ketone), a thiocarbonyl (such as a thioester, a thioacetate, or a thioformate), an amino, an acylamino, an amido, a cyano, a nitro, an azido, a sulfate, a sulfonate, a sulfonamido, $-(CH_2)_m-R_8$, $-(CH_2)_m-OH$, $-(CH_2)_m-O$ -lower alkyl, $-(CH_2)_m-O$ -lower alkenyl, $-(CH_2)_n-O-(CH_2)_m-R_8$, $-(CH_2)_m-SH$, $-(CH_2)_m-S$ -lower alkyl, $-(CH_2)_m-S$ -lower alkenyl, $-(CH_2)_n-S-(CH_2)_m-R_8$;

25 R_8 represents a substituted or unsubstituted aryl, aralkyl, cycloalkyl, cycloalkenyl, or heterocycle; and

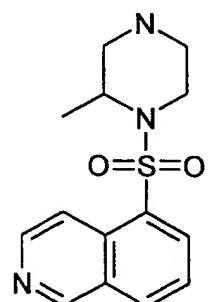
20 n and m are independently for each occurrence zero or an integer in the range of 1 to 6.

In a preferred embodiment, the PKA inhibitor is N-[2-((p-bromocinnamyl)amino)ethyl]-5-isoquinolinesulfonamide (H-89; Calbiochem Cat. No. 371963), e.g., having the formula:

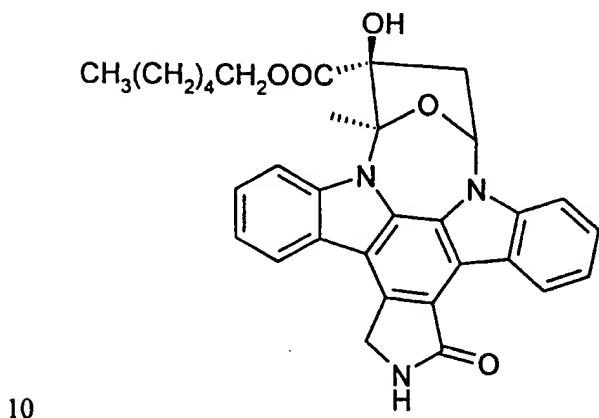


In another embodiment, the PKA inhibitor is 1-(5-isoquinolinesulfonyl)-2-methylpiperazine (H-7; Calbiochem Cat. No. 371955), e.g., having the formula:

5

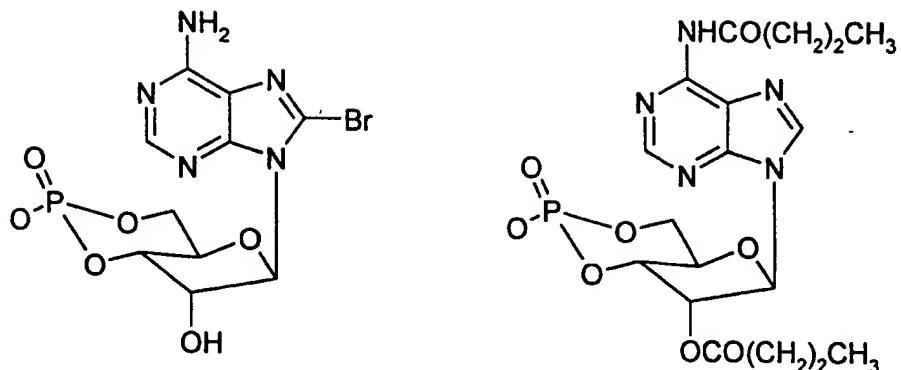


In still other embodiments, the PKA inhibitor is KT5720 (Calbiochem Cat. No. 420315), having the structure



10

A variety of nucleoside analogs are also useful as PKA inhibitors. For example, the subject method can be carried out cyclic AMP analogs which inhibit the kinase activity of PKA, as for example, 8-bromo-cAMP or dibutyryl-CAMP



Exemplary peptidyl inhibitors of PKA activity include the PKA Heat Stable Inhibitor (isoform α ; see, for example, Calbiochem Cat. No. 539488, and Wen et al. 5 (1995) *J Biol Chem* 270:2041).

Certain *hedgehog* receptors may stimulate the activity of phospholipases. Inositol lipids can be extracted and analyzed using standard lipid extraction techniques. Water soluble derivatives of all three inositol lipids (IP₁, IP₂, IP₃) can also be quantitated using radiolabelling techniques or HPLC.

10 The mobilization of intracellular calcium or the influx of calcium from outside the cell may be a response to *hedgehog* stimulation or lack thereof. Calcium flux in the reagent cell can be measured using standard techniques. The choice of the appropriate calcium indicator, fluorescent, bioluminescent, metallochromic, or Ca⁺⁺-sensitive microelectrodes depends on the cell type and the magnitude and time constant 15 of the event under study (Borle (1990) *Environ Health Perspect* 84:45-56). As an exemplary method of Ca⁺⁺ detection, cells could be loaded with the Ca⁺⁺-sensitive fluorescent dye fura-2 or indo-1, using standard methods, and any change in Ca⁺⁺ measured using a fluorometer.

20 In certain embodiments of the assay, it may be desirable to screen for changes in cellular phosphorylation. As an example, the drosophila gene *fused* (fu) which encodes a serine/threonine kinase has been identified as a potential downstream target in *hedgehog* signaling. (Preat et al., 1990 *Nature* 347, 87-89; Therond et al. 1993, *Mech. Dev.* 44, 65-80). The ability of compounds to modulate serine/threonine kinase activation could be screened using colony immunoblotting (Lyons and Nelson (1984) 25 *Proc. Natl. Acad. Sci. USA* 81:7426-7430) using antibodies against phosphorylated serine or threonine residues. Reagents for performing such assays are commercially available, for example, phosphoserine and phosphothreonine specific antibodies which

measure increases in phosphorylation of those residues can be purchased from commercial sources.

In yet another embodiment, the *ptc* therapeutic is an antisense molecule which inhibits expression of a protein involved in a *patched*-mediated signal transduction 5 pathway. To illustrate, by inhibiting the expression of a protein involved in *patched* signals, such as *fused*, *costal-2*, *smoothened* and/or *Gli* genes, or *patched* itself, the ability of the *patched* signal pathway(s) to alter the ability of, e.g., a dopaminergic or GABA-nergic cell to maintain its differentiated state can be altered, e.g., potentiated or repressed.

10 As used herein, "antisense" therapy refers to administration or *in situ* generation of oligonucleotide probes or their derivatives which specifically hybridize (e.g. bind) under cellular conditions with cellular mRNA and/or genomic DNA encoding a *hedgehog* protein, *patched*, or a protein involved in *patched*-mediated signal transduction. The hybridization should inhibit expression of that protein, e.g. by 15 inhibiting transcription and/or translation. The binding may be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, "antisense" therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

20 An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the target cellular mRNA. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell causes inhibition of expression by hybridizing 25 with the mRNA and/or genomic sequences of a target gene. Such oligonucleotide probes are preferably modified oligonucleotide which are resistant to endogenous nucleases, e.g. exonucleases and/or endonucleases, and is therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also 30 U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) *Biotechniques* 6:958-976; and Stein et al. (1988) *Cancer Res* 48:2659-2668.

35 Several considerations should be taken into account when constructing antisense oligonucleotides for the use in the methods of the invention: (1) oligos

should have a GC content of 50% or more; (2) avoid sequences with stretches of 3 or more G's; and (3) oligonucleotides should not be longer than 25-26 mers. When testing an antisense oligonucleotide, a mismatched control can be constructed. The controls can be generated by reversing the sequence order of the corresponding antisense 5 oligonucleotide in order to conserve the same ratio of bases.

In an illustrative embodiment, the *ptc* therapeutic can be an antisense construct for inhibiting the expression of *patched*, e.g., to mimic the inhibition of *patched* by *hedgehog*. Exemplary antisense constructs include:

5'-GTCCTGGCGCCGCCGCCGCCGCGTCGCC

10 5'-TTCCGATGACCGGCCTTCGCGGTGA

5'-GTGCACGGAAAGGTGCAGGCCACACT

VI. EXEMPLARY PHARMACEUTICAL PREPARATIONS OF HEDGEHOG AND PTC THERAPEUTICS:

15 The source of the *hedgehog* and *ptc* therapeutics to be formulated will depend on the particular form of the agent. Small organic molecules and peptidyl fragments can be chemically synthesized and provided in a pure form suitable for pharmaceutical/cosmetic usage. Products of natural extracts can be purified according to techniques known in the art. For example, the Cox et al. U.S. Patent 5,286,654 20 describes a method for purifying naturally occurring forms of a secreted protein and can be adapted for purification of *hedgehog* polypeptides. Recombinant sources of *hedgehog* polypeptides are also available. For example, the gene encoding *hedgehog* polypeptides, are known, *inter alia*, from PCT publications WO 95/18856 and WO 96/17924.

25 Those of skill in treating neural tissues can determine the effective amount of an *hedgehog* or *ptc* therapeutic to be formulated in a pharmaceutical or cosmetic preparation.

30 The *hedgehog* or *ptc* therapeutic formulations used in the method of the invention are most preferably applied in the form of appropriate compositions. As appropriate compositions there may be cited all compositions usually employed for systemically or locally (such as intrathecal) administering drugs. The pharmaceutically acceptable carrier should be substantially inert, so as not to act with the active component. Suitable inert carriers include water, alcohol polyethylene glycol, mineral oil or petroleum gel, propylene glycol and the like.

To prepare the pharmaceutical compositions of this invention, an effective amount of the particular *hedgehog* or ptc therapeutic as the active ingredient is combined in intimate admixture with a pharmaceutically acceptable carrier, which carrier may take a wide variety of forms depending on the form of preparation desired

5 for administration. These pharmaceutical compositions are desirable in unitary dosage form suitable, particularly, for administration orally, rectally, percutaneously, or by parenteral injection. For example, in preparing the compositions in oral dosage form, any of the usual pharmaceutical media may be employed such as, for example, water, glycols, oils, alcohols and the like in the case of oral liquid preparations such as

10 suspensions, syrups, elixirs and solutions; or solid carriers such as starches, sugars, kaolin, lubricants, binders, disintegrating agents and the like in the case of powders, pills, capsules, and tablets. Because of their ease in administration, tablets and capsules represents the most advantageous oral dosage unit form, in which case solid pharmaceutical carriers are obviously employed. For parenteral compositions, the

15 carrier will usually comprise sterile water, at least in large part, though other ingredients, for example, to aid solubility, may be included. Injectable solutions, for example, may be prepared in which the carrier comprises saline solution, glucose solution or a mixture of saline and glucose solution. Injectable suspensions may also be prepared in which case appropriate liquid carriers, suspending agents and the like may

20 be employed. Also included are solid form preparations which are intended to be converted, shortly before use, to liquid form preparations. In the compositons suitable for percutaneous administration, the carrier optionally comprises a penetration enhancing agent and/or a suitable wetting agent, optionally combined with suitable additives of any nature in minor proportions, which additives do not introduce a

25 significant deleterious effect on the skin.

It is especially advantageous to formulate the subject compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used in the specification and claims herein refers to physically discrete units suitable as unitary dosages, each unit containing a predetermined quantity of active ingredient

30 calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. Examples of such dosage unit forms are tablets (including scored or coated tablets), capsules, pills, powders packets, wafers, injectable solutions or suspensions, teaspoonfuls, tablespoonfuls and the like, and segregated multiples thereof.

35 The pharmaceutical preparations of the present invention can be used, as stated above, for the many applications which can be considered cosmetic uses. Cosmetic

compositions known in the art, preferably hypoallergic and pH controlled are especially preferred, and include toilet waters, packs, lotions, skin milks or milky lotions. The preparations contain, besides the *hedgehog* or ptc therapeutic, components usually employed in such preparations. Examples of such components are oils, fats, waxes, 5 surfactants, humectants, thickening agents, antioxidants, viscosity stabilizers, chelating agents, buffers, preservatives, perfumes, dyestuffs, lower alkanols, and the like. If desired, further ingredients may be incorporated in the compositions, e.g. antiinflammatory agents, antibacterials, antifungals, disinfectants, vitamins, sunscreens, antibiotics, or other anti-acne agents.

10 Examples of oils comprise fats and oils such as olive oil and hydrogenated oils; waxes such as beeswax and lanolin; hydrocarbons such as liquid paraffin, ceresin, and squalane; fatty acids such as stearic acid and oleic acid; alcohols such as cetyl alcohol, stearyl alcohol, lanolin alcohol, and hexadecanol; and esters such as isopropyl myristate, isopropyl palmitate and butyl stearate. As examples of surfactants there may 15 be cited anionic surfactants such as sodium stearate, sodium cetyl sulfate, polyoxyethylene lauryl ether phosphate, sodium N-acyl glutamate; cationic surfactants such as stearyl dimethylbenzyl ammonium chloride and stearyl trimethyl ammonium chloride; amphoteric surfactants such as alkylaminoethylglycine hydrochloride solutions and lecithin; and nonionic surfactants such as glycerin monostearate, sorbitan monostearate, sucrose fatty acid esters, propylene glycol monostearate, polyoxyethylene oleyl ether, polyethylene glycol monostearate, polyoxyethylene sorbitan monopalmitate, polyoxyethylene coconut fatty acid monoethanolamide, polyoxypropylene glycol (e.g. the materials sold under the trademark "Pluronic"), polyoxyethylene castor oil, and polyoxyethylene lanolin. Examples of humectants include glycerin, 1,3-butylene glycol, 20 and propylene glycol; examples of lower alcohols include ethanol and isopropanol; examples of thickening agents include xanthan gum, hydroxypropyl cellulose, hydroxypropyl methyl cellulose, polyethylene glycol and sodium carboxymethyl cellulose; examples of antioxidants comprise butylated hydroxytoluene, butylated hydroxyanisole, propyl gallate, citric acid and ethoxyquin; examples of chelating agents 25 include disodium edetate and ethanehydroxy diphosphate; examples of buffers comprise citric acid, sodium citrate, boric acid, borax, and disodium hydrogen phosphate; and examples of preservatives are methyl parahydroxybenzoate, ethyl parahydroxybenzoate, dehydroacetic acid, salicylic acid and benzoic acid.

30

For preparing ointments, creams, toilet waters, skin milks, and the like, typically 35 from 0.01 to 10% in particular from 0.1 to 5% and more in particular from 0.2 to 2.5% of the active ingredient, e.g., of the *hedgehog* or ptc therapeutic, will be incorporated in

the compositions. In ointments or creams, the carrier for example consists of 1 to 20%, in particular 5 to 15% of a humectant, 0.1 to 10% in particular from 0.5 to 5% of a thickener and water; or said carrier may consist of 70 to 99%, in particular 20 to 95% of a surfactant, and 0 to 20%, in particular 2.5 to 15% of a fat; or 80 to 99.9% in particular 5 90 to 99% of a thickener; or 5 to 15% of a surfactant, 2-15% of a humectant, 0 to 80% of an oil, very small (< 2%) amounts of preservative, coloring agent and/or perfume, and water. In a toilet water, the carrier for example consists of 2 to 10% of a lower alcohol, 0.1 to 10% or in particular 0.5 to 1% of a surfactant, 1 to 20%, in particular 3 to 7% of a humectant, 0 to 5% of a buffer, water and small amounts (< 2%) of 10 preservative, dyestuff and/or perfume. In a skin milk, the carrier typically consists of 10-50% of oil, 1 to 10% of surfactant, 50-80% of water and 0 to 3% of preservative and/or perfume. In the aforementioned preparations, all % symbols refer to weight by weight percentage.

Particular compositions for use in the method of the present invention are those 15 wherein the *hedgehog* or ptc therapeutic is formulated in liposome-containing compositions. Liposomes are artificial vesicles formed by amphiphatic molecules such as polar lipids, for example, phosphatidyl cholines, ethanolamines and serines, sphingomyelins, cardiolipins, plasmalogens, phosphatidic acids and cerebrosides. Liposomes are formed when suitable amphiphatic molecules are allowed to swell in 20 water or aqueous solutions to form liquid crystals usually of multilayer structure comprised of many bilayers separated from each other by aqueous material (also referred to as coarse liposomes). Another type of liposome known to be consisting of a single bilayer encapsulating aqueous material is referred to as a unilamellar vesicle. If water-soluble materials are included in the aqueous phase during the swelling of the 25 lipids they become entrapped in the aqueous layer between the lipid bilayers.

Water-soluble active ingredients such as, for example, various salt forms of a *hedgehog* polypeptide, are encapsulated in the aqueous spaces between the molecular layers. The lipid soluble active ingredient of *hedgehog* or ptc therapeutic, such as an organic mimetic, is predominantly incorporated into the lipid layers, although polar 30 head groups may protrude from the layer into the aqueous space. The encapsulation of these compounds can be achieved by a number of methods. The method most commonly used involves casting a thin film of phospholipid onto the walls of a flask by evaporation from an organic solvent. When this film is dispersed in a suitable aqueous medium, multilamellar liposomes are formed. Upon suitable sonication, the coarse 35 liposomes form smaller similarly closed vesicles.

Water-soluble active ingredients are usually incorporated by dispersing the cast film with an aqueous solution of the compound. The unencapsulated compound is then removed by centrifugation, chromatography, dialysis or other art-known suitable procedures. The lipid-soluble active ingredient is usually incorporated by dissolving it 5 in the organic solvent with the phospholipid prior to casting the film. If the solubility of the material in the lipid phase is not exceeded or the amount present is not in excess of that which can be bound to the lipid, liposomes prepared by the above method usually contain most of the material bound in the lipid bilayers; separation of the liposomes from unencapsulated material is not required.

10 A particularly convenient method for preparing liposome formulated forms of *hedgehog* and ptc therapeutics is the method described in EP-A-253,619, incorporated herein by reference. In this method, single bilayered liposomes containing encapsulated active ingredients are prepared by dissolving the lipid component in an organic medium, injecting the organic solution of the lipid component under pressure into an 15 aqueous component while simultaneously mixing the organic and aqueous components with a high speed homogenizer or mixing means, whereupon the liposomes are formed spontaneously.

20 The single bilayered liposomes containing the encapsulated *hedgehog* or ptc therapeutic can be employed directly or they can be employed in a suitable pharmaceutically acceptable carrier for localized administration. The viscosity of the 25 liposomes can be increased by the addition of one or more suitable thickening agents such as, for example xanthan gum, hydroxypropyl cellulose, hydroxypropyl methylcellulose and mixtures thereof. The aqueous component may consist of water alone or it may contain electrolytes, buffered systems and other ingredients, such as, for example, preservatives. Suitable electrolytes which can be employed include metal salts such as alkali metal and alkaline earth metal salts. The preferred metal salts are calcium chloride, sodium chloride and potassium chloride. The concentration of the electrolyte 30 may vary from zero to 260 mM, preferably from 5 mM to 160 mM. The aqueous component is placed in a suitable vessel which can be adapted to effect homogenization by effecting great turbulence during the injection of the organic component. Homogenization of the two components can be accomplished within the vessel, or, alternatively, the aqueous and organic components may be injected separately into a mixing means which is located outside the vessel. In the latter case, the liposomes are 35 formed in the mixing means and then transferred to another vessel for collection purpose.

The organic component consists of a suitable non-toxic, pharmaceutically acceptable solvent such as, for example ethanol, glycerol, propylene glycol and polyethylene glycol, and a suitable phospholipid which is soluble in the solvent. Suitable phospholipids which can be employed include lecithin, phosphatidylcholine, 5 phosphatidylserine, phosphatidylethanol-amine, phosphatidylinositol, lysophosphatidylcholine and phosphatidyl glycerol, for example. Other lipophilic additives may be employed in order to selectively modify the characteristics of the liposomes. Examples of such other additives include stearylamine, phosphatidic acid, tocopherol, cholesterol and lanolin extracts.

10 In addition, other ingredients which can prevent oxidation of the phospholipids may be added to the organic component. Examples of such other ingredients include tocopherol, butylated hydroxyanisole, butylated hydroxytoluene, ascorbyl palmitate and ascorbyl oleate. Preservatives such a benzoic acid, methyl paraben and propyl paraben may also be added.

15 Methods of introduction may also be provided by rechargeable or biodegradable devices. Various slow release polymeric devices have been developed and tested *in vivo* in recent years for the controlled delivery of drugs, including proteinaceous biopharmaceuticals. A variety of biocompatible polymers (including hydrogels), including both biodegradable and non-degradable polymers, can be used to form an 20 implant for the sustained release of an *hh* at a particular target site. Such embodiments of the present invention can be used for the delivery of an exogenously purified *hedgehog* protein, which has been incorporated in the polymeric device, or for the delivery of *hedgehog* produced by a cell encapsulated in the polymeric device.

25 An essential feature of certain embodiments of the implant can be the linear release of the therapeutic, which can be achieved through the manipulation of the polymer composition and form. By choice of monomer composition or polymerization technique, the amount of water, porosity and consequent permeability characteristics can be controlled. The selection of the shape, size, polymer, and method for 30 implantation can be determined on an individual basis according to the disorder to be treated and the individual patient response. The generation of such implants is generally known in the art. See, for example, *Concise Encyclopedia of Medical & Dental Materials*, ed. by David Williams (MIT Press: Cambridge, MA, 1990); and the Sabel et al. U.S. Patent No. 4,883,666.

35 In another embodiment of an implant, a source of cells producing the therapeutic, e.g., secreting a soluble form of a *hedgehog* protein, is encapsulated in

implantable hollow fibers or the like. Such fibers can be pre-spun and subsequently loaded with the cell source (Aebischer et al. U.S. Patent No. 4,892,538; Aebischer et al. U.S. Patent No. 5,106,627; Hoffman et al. (1990) *Expt. Neurobiol.* 110:39-44; Jaeger et al. (1990) *Prog. Brain Res.* 82:41-46; and Aebischer et al. (1991) *J. Biomech. Eng.* 113:178-183), or can be co-extruded with a polymer which acts to form a polymeric coat about the cells (Lim U.S. Patent No. 4,391,909; Sefton U.S. Patent No. 4,353,888; Sugamori et al. (1989) *Trans. Am. Artif. Intern. Organs* 35:791-799; Sefton et al. (1987) *Biotechnol. Bioeng.* 29:1135-1143; and Aebischer et al. (1991) *Biomaterials* 12:50-55).

10

EXEMPLIFICATION

The invention now being generally described, it will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention.

In *Drosophila*, the *hedgehog* gene was first discovered for the role it plays in early embryo patterning (Nusslein-Volhard and Wieschaus, 1980). Further study showed that the product of this gene is secreted, and as an intercellular signaling protein, plays a critical role in body segmentation and patterning of imaginal disc derivatives such as eyes and wings (Lee et al., 1992; Mohler and Vanie, 1992; Tabata et al., 1992). There are, at present, three mammalian homologues of *Drosophila* hedgehog, and Indian hedgehog (Fietz et al., 1994). During the course of vertebrate development, these secreted peptide molecules are involved in axial patterning, and consequently regulate the phenotypic specification of precursor cells into functional differentiated cells.

The embryonic expression pattern of Shh has been shown to be closely linked to the development and differentiation of the entire ventral neuraxis (Marti et al., 1995). Using naive neural tube explants derived from the appropriate levels of the rostrocaudal axis, it has been demonstrated that the induction of spinal motor neurons (Roelink et al., 1994; Tanabe et al., 1995), midbrain dopaminergic neurons (Hynes et al., 1995; Wang et al., 1995), and basal forebrain cholinergic neurons (Ericson et al., 1995) are dependent upon exposure to Shh. This molecule appears to be crucial for such patterning and phenotype specification *in vivo* since mouse embryos deficient in the expression of functional Shh gene product manifest a lack of normal ventral patterning in the central nervous system as well as gross atrophy of the entire cranium (Chiang et al., 1996).

In this study we have explored the issue of whether Shh may have activities at stages in neural development later than those previously studied. Namely, we have asked whether Shh is trophic for particular neural populations, and under toxic conditions, whether Shh is neuroprotective. Using cultures derived from the embryonic 5 day 14-16 (E14-16) rat, we find that Shh is trophic for midbrain, striatal, and spinal neurons. In the first case the factor is trophic for both dopaminergic and GABA-immunoreactive (GABA-ir) neurons. From the striatum, the surviving neurons are exclusively GABA-ir, while in the spinal cultures Shh promotes survival of a heterogeneous population of putative interneurons. Shh does not support survival of any 10 peripheral nervous system neurons tested. Finally, we show that Shh protects cultures of midbrain dopaminergic neurons from the toxic effects of MPP+, a specific neurotoxin that induces Parkinsonism *in vivo*. Together, these observations indicate a novel role for Shh in nervous system development and its potential role as a therapeutic.

15

MATERIALS AND METHODS

Whole-mount in situ hybridization

Whole-mount *in situ* hybridization on bisected E14.5 Sprague-Dawley rat embryos was performed with digoxigenin-labeled (Boehringer-Mannheim) mouse RNA 20 probes as previously described (Wilkinson, 1992). Bound probe was detected with alkaline phosphatase-conjugated anti-digoxigenin Fab fragments (Boehringer-Mannheim). The 0.7 kb *Shh* probes were transcribed using T3 (antisense) or T7 (sense) RNA polymerase from *Hind III* (antisense) or *Bam HI* (sense) linearized templates as described by Echelard, et al. (1993). The 0.9 kb *Ptc* probes were transcribed using T3 25 (antisense) or T7 (sense) RNA polymerase from *Bam HI* (antisense) or *Hind III* (sense) linearized templates as described by Goodrich, et al. (1996).

Shh protein and anti-Shh antibody

Rat sonic hedgehog amino terminal signaling domain (amino acids 2-198) 30 Porter et al., 1995) was cloned into a baculovirus expression vector (Invitrogen; San Diego, CA) (virus encoding Shh insert was a gift of Dr. Henk Roelink, University of Washington, Seattle, WA). High Five™ insect cells (Invitrogen) were infected with the baculovirus per manufacturer's instructions. The culture supernatant was batch adsorbed to heparin agarose type I (Sigma; St. Louis, MO) and Shh eluted with PBS containing a total of 0.75 M NaCl and 0.1- mM -mercaptoethanol. Shh concentration 35 was determined by the method of Ericson, et al. (1996). E. coli-derived Shh was

obtained as previously described (Wang et al., 1996) and purified as described above. All samples were sterile filtered and aliquots frozen in liquid nitrogen. Anti-Shh polyclonal antibody was a gift from Dr. Andy McMahon (Harvard University). Preparation of this reagent, directed against the amino peptide of Shh, is described by 5 Bumcrot et al. (1995). Anti-Shh monoclonal antibody (511) was a gift of Dr. Thomas Jessell (Columbia University), and preparation of this reagent is described by Ericson et al. (1996).

Dissociation and culture of neural tissue

E14.5 rat ventral mesencephalon was dissected as described by Shimoda, et al. 10 (Shimoda et al., 1992). Striatal cultures were established from E15-16 embryos from the regions identified by Altman and Bayer (1995) as the striatum and pallidum. Spinal cultures utilized the ventral one-third of the E15-16 spinal cord (Camu and Henderson, 1992). Tissues were dissociated for approximately 40 minutes in 0.10-0.25% trypsin-EDTA (Gibco/BRL; Gaithersburg, MD), and the digestion stopped using an equal 15 volume of Ca⁺⁺/Mg⁺⁺-free Hanks' buffered saline (Gibco/BRL) containing 3.5 mg/ml soybean trypsin inhibitor (Sigma) and 0.04% DNase (Grade II, Boehringer Mannheim; Indianapolis, IN). Cells were then plated at 2 x 20⁵ - 3 x 20⁵ cells/well in the medium of Kriegstein, et al. (1995) (a modified N2 medium) in 34-well tissue culture plates (Falcon) coated with poly-L-lysine or poly-L-ornithine (Sigma) after 2 wash in the same 20 medium. Note that this procedure results in cultures in which the cells have never been exposed to serum and stands in contrast to cultures in which serum has been used to neutralize dissociation proteases, and/or to intially "prime" the cells prior to serum withdrawal. The following peptide growth factors were added as indicated in the 25 results: basic fibroblast growth factor (FGFb), transforming growth factor 1(TGF 1), TGF 2, glia derived neurotrophic factor (GDNF), and brain derived neurotrophic factor (BDNF) (all from PeproTech; Rocky Hill, NJ; additional lots of BDNF and GDNF were purchased from Promega; Madison WI). Anti-TGF antibodies were purchased from R & D Systems. Antibody was added at the time of Shh addition to the cultures. Cultures were maintained for up to 3 weeks and the medium changed every 4 days.

30 *Immunocytochemistry and cell scoring*

For all cell staining, cultures were fixed with 5% paraformaldehyde in PBS (plus 0.1% glutaraldehyde if staining for GABA), and blocked using 3% goat serum, (Sigma), 0.1% Triton X-100, in PBS. Antibody incubations were performed in the 35 blocking solutions. Antibodies used in this study were anti-tubulin III (Sigma), anti-tyrosine hydroxylase (TH) (Boehringer-Mannheim), anti-GABA (Sigma), and anti-glial

fibrillary acidic protein (GFAP) (Sigma). Primary antibodies were detected using horseradish peroxidase-, alkaline phosphatase-, or flurochrome-conjugated secondary antibodies (Vector; Burlingame, CA). Peroxidase-linked secondaries were visualized using a NI/DAB kit (Zymed; South San Francisco, CA) and phosphatase-linked secondaries using Vector Blue™ (Vector).

Cell counting was performed using an Olympus inverted microscope at a total magnification of 30OX. Data presented are representative, and have been confirmed by repeating the cultures at least 4-10 independent times for each neural population discussed. Cell numbers are reported as cells/field (the average of 30-40 fields from a total of 5 wells/condition; 4-10 independent experiments were assessed for each culture condition examined). Consistency of counting was verified by at least 3 observers. Errors are reported as standard error of the mean (s.e.m.), and significance calculated by student's t-test.

Measurement of dopamine transport

To detect the presence of the dopamine transporter (Cerruti et al., 1993; Ciliax et al., 1995) cultures were incubated with a mixture consisting of: 5×10^{-8} M 3 H-dopamine (Amersham; Arlington Heights, IL; 48 Ci/mmol), 100 μ M ascorbic acid (Sigma), 1 μ M fluoxetine (Eli Lilly; Indianapolis, IN), 1 μ M desmethylimipramine (Sigma), and 10 μ M pargyline (Sigma) in DME-F12. Nonspecific labeling was measured by the addition of 5×10^{-5} M unlabeled dopamine. Cells were incubated for 30 minutes at 37 C, rinsed three times with PBS and processed for either scintillation counting or autoradiography. For scintillation counting cells were first lysed with 150 μ l of 0.1% SDS and then added to 500 μ l of Microscint 20 (Packard; Meriden, CT) and counted in a Packard Instrument Topcount scintillation machine. For autoradiography, sister plates were coated with NTB-2 autoradiographic emulsion (Kodak; Rochester, NY) that had been diluted 1:3 with 10% glycerol. The plates were then air dried, exposed for 1-2 weeks, and developed.

Quantitative-competitive polymerase chain reaction (QC-PCR)

RNA was isolated from cells and tissue using Trizol (Gibco/BRL) as prescribed by the manufacturer. Genomic DNA was removed from the RNA by incubation with 0.5 units of Dnase (Gibco/BRL, Cat # 28068-015) at room temperature for 25 minutes. The solution was heated to 75 C for 20 minutes to inactivate the DNase. Reverse transcription was carried out using random hexamer and MuLV reverse transcriptase (Gibco/BRL) as suggested by the manufacturer. All the quantitative RT-PCR internal controls, or mimics, were synthetic single stranded DNA oligonucleotides

corresponding to the target sequence with an internal deletion from the central region (Oligos, Etc.; Wilsonville, OR). For actin, target = 280 bp, mimic = 230 bp; for *ptc*, target = 354 bp, mimic = 200 bp. PCR was performed using the Clontech PCR kit. For actin: annealing temperature 64 °C, oligos GGCTCCGGTATGTGC,
5 GGGGTACTTCAGGGT. For *ptc*: annealing temperature 72 °C, oligos CATTGGCAGGAGGGAGTTGATTGTGG, AGCACCTTTGAGTG-AGTTGGGG. In each QC-PCR reaction, four reactions were set up with equal amounts of sample cDNA in each tube and 5-fold serial dilution of mimic. Also, for each sample an aliquot of cDNA was saved and amplified along with quantitative PCR as control for 10 contamination. PCR reactions were carried out in an MJ Research PTC-200 thermal cycler and the following cycling profile used: 95 °C for 45 seconds, 64 or 72 °C for 35 seconds, 82 °C for 30 seconds; for 40 cycles. The reaction mixtures were then fractionated by agarose electrophoresis, negative films obtained, and the films digitally scanned and quantified by area integration according to established procedures (Wang 15 et al., 1995, and references therein). The quantity of target molecules was normalized to the competing mimic and expressed as a function of cDNA synthesized and used in each reaction.

N-methyl-4-phenylpyridinium (MPP⁺) administration

Culture and MPP⁺ treatment of dopaminergic neurons were performed as 20 previously described (Hyman et al., 1994; Kriegstein et al., 1995). MPP⁺ (Aldrich; St. Louis, MO) was added at day 3 of culture to a final concentration of 3 µM for 58 hours. Cultures were then washed extensively to remove MPP⁺, cultured for an additional 34-48 hours to allow clearance of dying TH⁺ neurons, and then processed for immunocytochemistry.

25

RESULTS

Shh and Ptc Continue to be Expressed in the Rat CNS After the Major Period of Dorsoventral Patterning

Previous studies have shown that *shh* is expressed in the vertebrate embryo in 30 the period during which dorsoventral patterning manifests (approximately E9-10 in the rat). Within the central nervous system, *shh* expression persists beyond this period and can be detected at a very high level in the E14-16 rat embryo. For example, in situ hybridization studies of the E14.5 embryo (Fig. 1A and E) reveal that *shh* is expressed in ventral regions of the spinal cord, hindbrain, midbrain, and diencephalon. Lower 35 levels of expression are observed in the ventral striatum and septum, while no

expression is observed in the cortex within the limits of detection of this method. Interestingly, a "streak" of *shh* expression (Fig. 1A, arrow) is observed to bisect the diencephalon into rostral and caudal halves. This is likely to be the zona limitans intrathalamica that separates prosomeres 2 and 3, and has been previously observed in 5 the studies of *shh* expression in the developing chick embryo (Marti, et al., 1995).

Recent biochemical evidence supports the view that the *ptc* gene product can act as a high affinity Shh receptor (Marigo et al., 1996a; Stone et al., 1996). *Ptc* shows a complementary pattern of expression (Fig. 1C and E), and is observed primarily lateral and dorsal to the sites of *shh* expression. The complementarity of expression is most 10 dramatic in the diencephalon where *ptc* mRNA is absent from the zona limitans, but is expressed at a very high level on either side of this structure. Of further interest is the observation that rostral of the zonal limitans, *ptc* expression no longer seems as restricted to regions immediately dorsal of *shh* expression. Again, within the detection 15 limits of this technique, *ptc* is not expressed in the cortex. Thus in regions where *shh* is expressed, adjacent tissue appears capable of responding to the gene product as evidenced by expression of the putative receptor.

Shh Promotes Dopaminergic Neuron Survival

In the developing midbrain (E9), Shh was first characterized for its ability to induce the production of dopaminergic neurons. Thus the trophic potential of Shh was 20 tested on this neuronal population at a stage when these neurons have already been induced. Using cultures derived from the E14.5 mesencephalon it was found that Shh increases the survival of TH+ neurons in a dose dependent manner (Fig. 2A). These cells exhibited a neuronal morphology (Fig. 2B), and greater than 95% of the TH+ cells were also positive for the neuron-specific marker, tubulin III (Banerjee et al., 1990); 25 GFAP staining revealed no glial cells (data not shown). Differences in TH+ neuron survival between control and Shh treated wells could be observed as early as 5 days. Note that under these stringently serum-free conditions (i.e. at no time were the cells exposed to serum), baseline levels of survival are even lower than those conventionally reported for cultures that have been maintained in low serum or that have been briefly 30 serum "primed". By 3 weeks in culture less than 6% of the total TH+ cells plated were present in the control condition, whereas 35-30% survive at 60 ng/ml of Shh (from 5 to 24 days, p<.001 at 35 and 60 ng/ml).

All catecholaminergic neurons express TH, but the presence of a specific high affinity DA uptake system is indicative of midbrain dopaminergic neurons (Di Porzio et 35 al., 1980; Denis-Donini et al., 1984; Certuti et al., 1993; Ciliax et al., 1995). As further

evidence that the cells supported by Shh are *bona fide* dopaminergic neurons, specific, high affinity dopamine (DA) uptake was also demonstrated (Figure 3). Midbrain cultures treated with Shh transported and retained 3 H-DA with a dose response profile paralleling that of survival curves (Fig. 3A) ($p<0.005$ at 25 and 50 ng/ml). Emulsion autoradiography also demonstrated that the cells taking up 3 H-DA were neuronal in morphology (Fig. 3B). In addition, immunohistochemistry for dopamine itself demonstrated high cellular content (data not shown).

The observed effect of Shh on increased TH+ neuron number is unlikely to be due to differentiation of latent progenitor cells since previous studies demonstrated that 10 the ability of Shh to induce dopaminergic neurons in explanted tissue is lost at later stages of development (Hynes et al., 1995; Wang et al., 1995). Furthermore, the effects are unlikely to be due to a mitogenic response of committed neuroblasts since pulsing the cultures with 5-brom-2'-deoxyuridine (BrdU) at 1, 2, or 4 days *in vitro* revealed very low mitotic activity in the presence or absence of Shh (data not shown). Thus in 15 addition to inducing dopaminergic neurons in the naive mesencephalon, Shh is a trophic factor for these neurons.

Specificity of Shh Action on Midbrain Neurons: Regulated expression of Ptc

Expression of *ptc* has previously been shown to be regulated by Shh (Goodrich et al., 1996; Marigo et al., 1996b), and to date, Shh is the only factor known to 20 transcriptionally upregulate *ptc* expression. Therefore, the expression of *ptc* by mesencephalic explants would reinforce the view that these cells are capable of responding to Shh, and upregulation of *ptc* mRNA in response to Shh would strongly indicate the specificity of such a response. Therefore, quantitative competitive PCR (QC-PCR) was used to measure the level of *ptc* expression.

25 *Ptc* mRNA levels were measured at 0, 3, 5, and 7 days of culture by the method described by Wang, et al. (1995). For each culture condition at each timepoint, 5 separate cDNA samples were co-amplified with a different known amount of mimic substrate (DNA that can be amplified by the same primers but yielding a product of molecular weight lower than that being sought in the sample). Thus for each condition 30 and timepoint, a gel like that shown in Fig. 4A was generated (upper bands correspond to amplified *ptc* transcripts; lower bands correspond to amplified mimic). Using a scanning densitometer to quantify the observed bands, a graph was produced for each sample (Fig. 4B corresponds to Fig. 4A). When the density of the target band and the mimic band are equal, the concentration of the unknown target can be taken to be equal 35 to the known concentration of mimic. Based on a linear curve fit, the concentration of

mimic at the point at which the density of the mimic and the target substrate are equal ($\text{Log Ds/Dm} = 0$) was taken to be the concentration of the substrate in the sample; this value was then normalized to the total amount of cDNA added to the reaction. These values are plotted in Fig. 4C; correlation coefficients (r^2) of the curve fits always 5 exceeded 0.95, and thus the margin of error for the values presented is less than 5%. This experiment was performed two independent times with independent cultures and the results were nearly identical.

As shown in Fig. 4C, significant *ptc* expression was observed in the E14.5 ventral mesencephalon (time 0). After two days of culture, higher levels of *ptc* 10 expression were observed than at the time of dissection; in control cultures this might reflect the loss of *ptc* non-expressing cell types since a constant amount of RNA was analyzed. There was no difference in *ptc* expression between control cultures and those treated with either 5 or 25 ng/ml of Shh at this time. However, cultures treated with 50 ng/ml of Shh showed a 20-fold induction of *ptc* mRNA expression relative to time of 15 dissection and at least 5-fold over other culture conditoin. By 5 days of culture, *ptc* message levels had declined significantly in comparison to the 3 day level of expression but high levels of expression were still observed in 50 ng/ml Shh. By 7 days, no *ptc* expression was obsesrvd in either the control or 5 ng/ml Shh treated cultures, although actin could still be detected (data not shown). It is important to note that in the 25 and 20 50 ng/ml Shh-treated cultures *ptc* expression matched or exceeded the time zero expression of *ptc* in the mescencephalon despite the overall decrease in cell number. These results indicate that: A) *ptc* is expressed in the E14.5 ventral mesencephalon (suggesting that the cells in this region are capable of responding to Shh), b) Shh is necessary for the maintenance of *ptc* gene expression, and c) that the expression of *ptc* 25 shows a Shh dose dependence that parallels the neurotrophic activity described above.

Specificity of Shh Action on Midbrain Neurons: Immunoneutralization

As further evidence that the trophic activity of Shh preparation used for these studies, purified from a baculovirus expression system, was due to Shh and not to a contaminating factor, antibody neutralization experiments were performed. As shown 30 in Fig. 4D, a saturating dose of Shh (50 ng/ml) promotes midbrain neuron survival ($p < .001$) while the same dose of Shh in the presence of a 5-fold molar excess of activity-neutralizgin, anti-Shh, monoclonal antibody (5E1; Ericson, et al. (1996)) inhibits this trophic response ($p < .001$). In earlier studies (data not shown), an affinity purified, polyclonal, anti-Shh antibody dramatically reduced the activity of Shh in the 35 dopaminergic neuron survival assay ($p < .005$), whereas purified rabbit IgG antibody from preimmune sera had no significant effect. Anti-TGF antibodies used at a 3-fold

molar excess to Shh did not inhibit the trophic activity, while they did inhibit the previously reported (Krieglestein et al., 1995) trophic effects of exogenously applied TGF s (data not shown). Addition of -galactosidase, expressed and purified in a manner identical to Shh, failed to show any trophic effect (data not shown), and thus 5 renders unlikely the possibility that an undefined baculovirus protein iss responsible for the observed trophic effects. Finally, Shh purified from an *E. coli* expression system (Wang et al., 1995) also had trophic activity for TH+ cells, while -galactosidase purified identically to Shh from the *E. coli* expression system gave no such activity even at concentrations as high as 20 μ g/ml (data not shown).

10 *Shh supports the Survival of other Midbrain Neurons*

Since the original observations concerning the role of Shh in midbrain development were concerned with induction of dopaminergic neurons (Hynes et al., 1995; Want et al., 1995), the current study initially focused on possible trophic effects on these neurons. Interestingly, the cultures in which the above described trophic 15 effects were observed, also demonstrated that the trophic effect of Shh extended to non-dopaminergic neurons (i.e. TH neurons). Within the dopaminergic neucleus of the midbrain, the substantia nigra, GABA is also a major neurotransmitter (Masuko et al., 1992). Staining for GABA in these cultures (Fig. 5) showed that GABA+ cells are supported by the presence of Shh with a dose response profile comparable to TH+ cells. 20 Furthermore, GABA cells outnumbered TH+ cells by a ratio of approximately 3.1. The two cell types together account for approximately 95% of the total neurons as gauged by staining for tubulin III (data not shown), and thus it is clear that the trophic effect of Shh on midbrain neurons extends to multiple neuron subtypes (for TH, $p < 0.001$ at 35 and 60 ng/ml; for GABA, $p < .001$ at 35 and 60 ng/ml).

25 *Shh Effects on Striatal Neurons*

Since Shh is strongly expressed in the ventral and lateral forebrain (Echelard et al., 1993; Ericson et al., 1995), and that the Shh knockout mouse exhibits triatal defects (Chiang et al., 1996), Shh neurotrophic activity was examined in striatum-derived cultures as well. As assessed after 4 days *in vitro* (Fig. 6), Shh is a potent trophic factor 30 for neurons cultured from the E15-16 striatum, and shows a dose response comparable to that of the midbrain. In comparing the number of total neurons (tubulin III+ cells) with that of GABA+ neurons, it is clear that essentially all of the neurons supported by Shh are GABA-nergic (fig. 6) (tubulin III, $p < 0.001$ at 25 and 50 ng/ml; GABA, $p < .001$ at 25 and 50 ng/ml). That this effect is trictly trophic was confirmed by the 35 observation that BrdU labeling indices over the course of the culture period were low

and did not vary with dose (data not shown). Closer inspection reveals that the intensity of GABA staining is variable, and it is thus possible that various subtypes of GABA+ interneurons (reviewed by Kawaguchi et al., 1995) are all supported by Shh.

Shh Effects on Spinal Neurons

5 As a further examination of the postinductive effectives of Shh on ventral neural tube derivatives, cultures of the E14-15 ventral neural tube were cultured with varying amounts of Shh. Again, with a dose response identical to that observed in the mesencephalic and striatal cultures, Shh promotes the survival of tubulin III+ neurons as scored after 4 days *in vitro* (Fig. 6A). A majority, but not all of these cells also stain
10 for GABA, and a smaller subset stain for a nuclear marker of spinal interneurons, Lim-1/2 (Tsuchida et al., 1994) (Fig 6A-C) (tubulin III, p < 0.001 at 25 and 50 ng/ml; Lim-1/2, p < .001 at 5, 10, 25 and 50 ng/ml; GABA, p .001 at 25 and 50 ng/ml). It is important to note that while there is overlap between the GABA+ and Lim-1/2+ populations, the latter is not merely a subset of the former since there are Lim-1/2+
15 cells that do not stain for GABA. Interestingly, immunoreactivity for the low affinity nerve growth factor receptor (Camu and Henderson, 1992), Islet-1 (Ericson et al., 1992), or galectin-1 (Hynes et al., 1990), all markers of rat motoneurons, was not detectable in these cultures, and thus it appears that Shh is not trophic for spinal motoneurons.

20 *Shh Protects Th+ Cells Against MPP+ Toxicity*

The toxin, 5-phenyl-1,2,3,6-tetrahydroptazine (MPTP), and its active metabolite, MPP+, are selectively toxic to mesencephalic dopaminergic neurons (Kopin and Markey, 1988; Forno et al., 1993). Since other agents that promote survival of TH+ cells also protect against chemical toxicity of MPP+ (Hyman et al., 1991; Kriegstein et al., 1995), we tested the ability of Shh to protect TH+ cells in E14 rat mesencephalon explants from the effects of MPP+. As shown in Figure 8, the presence of Shh in cultures treated for 58 hours with MPP+ significantly increased the numbers of TH+ cells that were observed in culture after removal of the MPP+. MPP+ treatment caused a greater than 90% reduction in the numbers of TH+ cells compared to non-MPP+
25 treated control cultures, whereas incubation with Shh protected the Th+ cells so that only a 75% reduction of TH+ cells occurred after MPP+ treatment versus controls. Suster cultures tested for 4H-DA transport demonstrated a 8-fold increase in transport
30 in Shh treated cultures versus controls (data not shown).

35 Shh was significantly more active in protecting TH+ cells from the effects of MPP+ than the other growth factors tested: glia-derived neurotrophic factor (GDNF)

(Lin et al., 1993) and brain-derived neurotrophic factor (BDNF) (Hyman et al., 1991) (Shh, $p < 0.001$ at 60 and 350 ng/ml; BDNF no significance; GDNF, $p < .05$). In the serum free conditions used in these experiments, none of the other growth factors tested showed as significant a level of TH+ cell protection from MPP+ toxicity as Shh, even 5 when tested at levels previously shown to be optimal for neuroprotection (Fig. 8).

DISCUSSION

Shh is Neurotrophic for a Variety of Ventral Neurons

The hypothesis that Shh may play roles in the nervous system in addition to its 10 initial function in neural tube ventralization was first suggested by the observation that Shh expression in ventral neural tissue along the entire neuraxis continues well past the period during which phenotypic specification has occurred (Echelard et al., 1993). Moreover, preliminary evidence generated in our laboratory indicates the presence of 15 significant levels of Sh mRNA in specific regions of the adult human-CNS (e.g. spinal cord and substantia nigra, P. Jin, unpublished observations). We report here the first evidence that Shh can indeed exert effects independent of its induction and patterning activity.

Unlike its role at earlier stages of neural development, this novel neurotrophic 20 activity acts on postmitotic neurons rather than on dividing progenitor cells. While the general trophic effect is apparent in a number of CNS regions (Fig. 2 and 6-7), there are both differences and similarities in the effects observed among the regions examined. Given the fact that Shh is necessary for the induction of both spinal motor neurons and 25 midbrain dopaminergic neurons, one might predict that Shh would be subsequently trophic for the cells. Strikingly, Shh is a very potent trophic factor for the midbrain dopaminergic neurons (Fig. 2), but in the cultures of ventral spinal neurons, no such 30 effect on motor neurons was observed. Thus there is no direct correlation between the neuron phenotypes induced by Shh, and those supported by Shh in a trophic manner. Interestingly, a common feature among the three CNS regions examined was the trophic effect for GABA-ergic neurons (Fig. 6-7). While it is not obvious whether these specific GABA+ populations are directly or indirectly induced by Shh during 35 early development (cf. Pfaff et al., 1996), it is plausible that the trophic actions on these neurons are direct.

It is important to note that the neurotrophic effects reported herein are not lacking in specificity. For example, neurons of the peripheral nervous system show no 35 survival in response to Shh administration, and preliminary studies of cultures derived

from E15-16 dorsal CNS regions (e.g. neocortex and dorsal spinal cord) show high baseline levels of neuron survival with no significant response to exogenous Shh application (J.A.O. and N.K.M., unpublished observation). Thus there appears to be a general restriction of the trophic effects of Shh to regions of the CNS specified by Shh, 5 but the actual targets of trophic activity need not encompass the phenotypes whose induction is Shh-dependent. Nevertheless, the fact that Shh also protects neurons from toxic insult (Fig. 8), suggests previously unforeseen therapeutic roles for Shh as well.

Possible Mechanisms of Shh Action

As stated above, the neurotrophic effect of Shh observed in these cultures is not 10 due to the stimulation of proliferation. One could argue, however, that the observed effects are indirect. In one scenario, Shh may act on a non-neuronal cell that in turn responds by secreting a neurotrophic factor. We observed no sign of astrocytes in any of our neural cultures, either by morphology or by staining for GFAP. Furthermore, in 15 the purely neuronal cultures established from the midbrain, *ptc* is greatly upregulated in response to Shh, and thus the reported survival effects must be due to a response by neurons (Fig. 4C).

In another scenario, it is possible that Shh acts directly on some or all of the 20 neurons, but the response is to secrete another factor(s) that actually possesses the survival activity. For example, Shh has been shown to induce the expression of TGF family members such as BMP's *in vivo* (Laufer et al., 1994; Levin et al., 1995) and 25 these proteins are trophic for midbrain dopaminergic neurons (Krieglstein et al., 1995). That induced expression of TGF's is the trophic mechanism seems unlikely since exogenous TGF's show only modest trophic activity in our culture system, and the presence of neutralizing, anti-pan-TGF antibodies failed to inhibit the neurotrophic 30 effects of Shh. Thus, at a minimum, Shh supports the survival of a subset of ventral CNS neurons. The mechanism by which Shh supports neuron survival is yet to be determined. While we favor the hypothesis that these trophic effects are direct, it remains possible that the survival response is due to Shh-induced expression of a secondary trophic factor.

As in the case of many secreted peptide factors, it now appears that Shh has 35 activities that can vary greatly depending on the spatiotemporal context in which the factor is expressed. While it was initially thought that the primary role of Shh in the CNS is in early patterning events that are critical to phenotypic specification, it is now clear that Shh can also contribute to the survival and maturation of these CNS regions. Interestingly, the cell types acted upon in these two distinct roles of Shh do not

necessarily overlap. Thus a more thorough understanding of this multifaceted molecule will require a better understanding of its patterns of expression beyond early embryogenesis. Moreover, it will be critical to ascertain the significance of the trophic effects of Shh *in vivo*.

5

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5 All of the above-cited references and publications are hereby incorporated by reference.

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the
5 following claims.

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1275

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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1				5					10						15		
25	TGC	GCT	CTT	TTA	GTC	TCC	TCT	GGG	CTG	ACT	TGT	GGA	CCA	GGC	AGG	GGC	96
	Cys	Ala	Leu	Leu	Val	Ser	Ser	Gly	Leu	Thr	Cys	Gly	Pro	Gly	Arg	Gly	
				20					25						30		
30	ATT	GGA	AAA	AGG	AGG	CAC	CCC	AAA	AAG	CTG	ACC	CCG	TTA	GCC	TAT	AAG	144
	Ile	Gly	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	
				35					40						45		
35	CAG	TTT	ATT	CCC	AAT	GTG	GCA	GAG	AAG	ACC	CTA	GGG	GCC	AGT	GGA	AGA	192
	Gin	Phe	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	
				50				55				60					
40	TAT	GAA	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAG	AGA	TTT	AAA	GAA	CTA	ACC	240
	Tyr	Glu	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	
				65				70				75			80		
45	CCA	AAT	TAC	AAC	CCT	GAC	ATT	ATT	TTT	AAG	GAT	GAA	GAG	AAC	ACG	GGA	288
	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	
				85				90							95		
50	GCT	GAC	AGA	CTG	ATG	ACT	CAG	CGC	TGC	AAG	GAC	AAG	CTG	AAT	GCC	CTG	336
	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	
				100				105							110		
55	GCG	ATC	TCG	GTG	ATG	AAC	CAG	TGG	CCC	GGG	GTG	AAG	CTG	CGG	GTG	ACC	384
	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Lys	Leu	Arg	Val	Thr	
				115				120							125		
60	GAG	GGC	TGG	GAC	GAG	GAT	GGC	CAT	CAC	TCC	GAG	GAA	TCG	CTG	CAC	TAC	432
	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	
				130				135				140					
	GAG	GGT	CGC	GCC	GTG	GAC	ATC	ACC	ACG	TCG	GAT	CGG	GAC	CGC	AGC	AAG	480
	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	
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	Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val	
	165 170 175	
5	TAC TAC GAG TCC AAG GCG CAC ATC CAC TGC TCC GTC AAA GCA GAA AAC	576
	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn	
	180 185 190	
10	TCA GTG GCA GCG AAA TCA GGA GGC TGC TTC CCT GGC TCA GCC ACA GTG	624
	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val	
	195 200 205	
	CAC CTG GAG CAT GGA GGC ACC AAG CTG GTG AAG GAC CTG AGC CCT GGG	672
	His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly	
	210 215 220	
15	GAC CGC GTG CTG GCT GCT GAC GCG GAC GGC CGG CTG CTC TAC AGT GAC	720
	Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp	
	225 230 235 240	
20	TTC CTC ACC TTC CTC GAC CGG ATG GAC AGC TCC CGA AAG CTC TTC TAC	768
	Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr	
	245 250 255	
25	GTC ATC GAG ACG CGG CAG CCC CGG GCC CGG CTG CTA CTG ACG GCG GCC	816
	Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala	
	260 265 270	
30	CAC CTG CTC TTT GTG GCC CCC CAG CAC AAC CAG TCG GAG GCC ACA GGG	864
	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly	
	275 280 285	
	TCC ACC AGT GGC CAG GCG CTC TTC GCC AGC AAC GTG AAG CCT GGC CAA	912
	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln	
	290 295 300	
35	CGT GTC TAT GTG CTG GGC GAG GGC GGG CAG CAG CTG CTG CCG GCG TCT	960
	Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser	
	305 310 315 320	
40	GTC CAC AGC GTC TCA TTG CGG GAG GAG GCG TCC GGA GCC TAC GCC CCA	1008
	Val His Ser Val Ser Leu Arg Glu Ala Ser Gly Ala Tyr Ala Pro	
	325 330 335	
45	CTC ACC GCC CAG GGC ACC ATC CTC ATC AAC CGG GTG TTG GCC TCC TGC	1056
	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys	
	340 345 350	
50	TAC GCC GTC ATC GAG GAG CAC AGT TGG GCC CAT TGG GCC TTC GCA CCA	1104
	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro	
	355 360 365	
55	TTC CGC TTG GCT CAG GGG CTG CTG GCC GCC CTC TGC CCA GAT GGG GCC	1152
	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala	
	370 375 380	
	ATC CCT ACT GCC GCC ACC ACC ACT GGC ATC CAT TGG TAC TCA CGG	1200
	Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg	
	385 390 395 400	
60	CTC CTC TAC CGC ATC GGC AGC TGG GTG CTG GAT GGT GAC GCG CTG CAT	1248
	Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His	
	405 410 415	

CCG CTG GGC ATG GTG GCA CCG GCC AGC TG
 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425 1277

5

(2) INFORMATION FOR SEQ ID NO:2:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1191

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG GCT CTG CCG GCC AGT CTG TTG CCC CTG TGC TGC TTG GCA CTC TTG 48
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15

30 GCA CTA TCT GCC CAG AGC TGC GGG CCG GGC CGA GGA CCG GTT GGC CGG 96
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30

35 CGG CGT TAT GTG CGC AAG CAA CTT GTG CCT CTG CTA TAC AAG CAG TTT 144
 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

40 GTG CCC AGT ATG CCC GAG CGG ACC CTG GGC GCG AGT GGG CCA GCG GAG 192
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

45 GGG AGG GTA ACA AGG GGG TCG GAG CGC TTC CGG GAC CTC GTA CCC AAC 240
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

50 TAC AAC CCC GAC ATA ATC TTC AAG GAT GAG GAG AAC AGC GGC GCA GAC 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

55 CGC CTG ATG ACA GAG CGT TGC AAA GAG CGG GTG AAC GCT CTA GCC ATC 336
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

60 GCG GTG ATG AAC ATG TGG CCC GGA GTA CGC CTA CGT GTG ACT GAA GGC 384
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

TGG GAC GAG GAC GGC CAC CAC GCA CAG GAT TCA CTC CAC TAC GAA GGC 432
 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140

CGT GCC TTG GAC ATC ACC ACG TCT GAC CGT GAC CGT AAT AAG TAT GGT 480

	Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly		
145	150	155	160
5	TTG TTG GCG CGC CTA GCT GTG GAA GCC GGA TTC GAC TGG GTC TAC TAC Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr 165 170 175		528
10	GAG TCC CGC AAC CAC ATC CAC GTA TCG GTC AAA GCT GAT AAC TCA CTG Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu 180 185 190		576
15	GCG GTC CGA GCC GGA GGC TGC TTT CCG GGA AAT GCC ACG GTG CGC TTG Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu 195 200 205		624
20	CGG AGC GGC GAA CGG AAG GGG CTG AGG GAA CTA CAT CGT GGT GAC TGG Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp 210 215 220		672
25	GTA CTG GCC GCT GAT GCA GCG GGC CGA GTG GTA CCC ACG CCA GTG CTG Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu 225 230 235 240		720
30	CTC TTC CTG GAC CGG GAT CTG CAG CGC CGC GCC TCG TTC GTG GCT GTG Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val 245 250 255		768
35	GAG ACC GAG CGG CCT CCG CGC AAA CTG TTG CTC ACA CCC TGG CAT CTG Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu 260 265 270		816
40	GTG TTC GCT GCT CGC GGG CCA GCG CCT GCT CCA GGT GAC TTT GCA CCG Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro 275 280 285		864
45	GTG TTC GCG CGC CGC TTA CGT GCT GGC GAC TCG GTG CTG GCT CCC GGC Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly 290 295 300		912
50	GGG GAC GCG CTC CAG CCG GCG CGC GTA GCC CGC GTG GCG CGC GAG GAA Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu 305 310 315 320		960
55	GCC GTG GGC GTG TTC GCA CCG CTC ACT GCG CAC GGG ACG CTG CTG GTC Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val 325 330 335		1008
60	AAC GAC GTC CTC GCC TCC TGC TAC GCG GTT CTA GAG AGT CAC CAG TGG Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp 340 345 350		1056
	GCC CAC CGC GCC TTC GCC CCT TTG CGG CTG CTG CAC GCG CTC GGG GCT Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala 355 360 365		1104
	CTG CTC CCT GGG GGT GCA GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser 370 375 380		1152
	CGC CTC CTT TAC CGC TTG GCC GAG GAG TTA ATG GGC TG Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly 385 390 395		1190

(2) INFORMATION FOR SEQ ID NO:3:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

10 10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1233

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG	TCT	CCC	GCC	TGG	CTC	CGG	CCC	CGA	CTG	CGG	TTC	TGT	CTG	TTC	CTG	48
Met	Ser	Pro	Ala	Trp	Leu	Arg	Pro	Arg	Leu	Arg	Phe	Cys	Leu	Phe	Leu	
1	5				10				15							
25	CTG	CTG	CTG	CTT	CTG	GTG	CCG	GCG	CGG	GGC	TGC	GGG	CCG	GGC	CGG	96
Leu	Leu	Leu	Leu	Leu	Val	Pro	Ala	Ala	Arg	Gly	Cys	Gly	Pro	Gly	Arg	
20				25					30							
30	GTG	GTG	GGC	AGC	CGC	CGG	AGG	CCG	CCT	CGC	AAG	CTC	GTG	CCT	GCC	144
Val	Val	Gly	Ser	Arg	Arg	Arg	Pro	Pro	Arg	Lys	Leu	Val	Pro	Leu	Ala	
35				35			40			45						
35	TAC	AAG	CAG	TTC	AGC	CCC	AAC	GTG	CCG	GAG	AAG	ACC	CTG	GGC	GCC	192
Tyr	Lys	Gln	Phe	Ser	Pro	Val	Asn	Pro	Asn	Val	Pro	Glu	Lys	Thr	Leu	
50					55					60						
40	GGG	CGC	TAC	GAA	GGC	AAG	ATC	GCG	CGC	AGC	TCT	GAG	CGC	TTC	AAA	240
Gly	Arg	Tyr	Glu	Gly	Lys	Ile	Ala	Arg	Ser	Ser	Glu	Arg	Phe	Lys	Glu	
65				65			70			75			80			
45	CTC	ACC	CCC	AAC	TAC	AAT	CCC	GAC	ATC	ATC	TTC	AAG	GAC	GAG	AAC	288
Leu	Thr	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	
85					85			90			95					
50	ACG	GGT	GCC	GAC	CGC	CTC	ATG	ACC	CAG	CGC	TGC	AAG	GAC	CGT	CTG	336
Thr	Gly	Ala	Asp	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Arg	Leu	Asn	
100					100			105			110					
55	TCA	CTG	GCC	ATC	TCT	GTC	ATG	AAC	CAG	TGG	CCT	GGT	GTG	AAA	CTG	384
Ser	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Gln	Trp	Pro	Gly	Val	Lys	Leu	
115					115			120			125					
55	GTG	ACC	GAA	GGC	CGG	GAT	GAA	GAT	GGC	CAT	CAC	TCA	GAG	GAG	TCT	432
Val	Thr	Glu	Gly	Arg	Asp	Glu	Asp	Gly	Gly	His	His	Ser	Glu	Glu	Ser	
130					130			135			140					
60	CAC	TAT	GAG	GGC	CGC	GCG	GTG	GAT	ATC	ACC	ACC	TCA	GAC	CGT	GAC	480
His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	Ser	Asp	Arg	Asp	Arg		
145					145			150			155			160		
60	AAT	AAG	TAT	GGA	CTG	CTG	GCG	CGC	TTA	GCA	GTG	GAG	GCC	GGC	TTC	528
Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	Ala	Val	Glu	Ala	Gly	Phe	Asp	

	165	170	175	
5	TGG GTG TAT TAC GAG TCC AAG GCC CAC GTG CAT TGC TCT GTC AAG TCT Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser 180 185 190			576
10	GAG CAT TCG GCC GCT GCC AAG ACA GGT GGC TGC TTT CCT GCC GGA GCC Glu His Ser Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala 195 200 205			624
15	CAG GTG CGC CTA GAG AAC GGG GAG CGT GTG GCC CTG TCA GCT GTC AAG Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys 210 215 220			672
20	CCA GGA GAC CGG GTG CTG GCC ATG GGG GAG GAT GGG ACC CCC ACC TTC Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe 225 230 235 240			720
25	AGT GAT GTG CTT ATT TTC CTG GAC CGC GAG CCA AAC CGG CTG AGA GCT Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala 245 250 255			768
30	TTC CAG GTC ATC GAG ACT CAG GAT CCT CCG CGT CGG CTG GCG CTC ACG Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr 260 265 270			816
35	CCT GCC CAC CTG CTC TTC ATT GCG GAC AAT CAT ACA GAA CCA GCA GCC Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala 275 280 285			864
40	CAC TTC CGG GCC ACA TTT GCC AGC CAT GTG CAA CCA GGC CAA TAT GTG His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val 290 295 300			912
45	CTG GTA TCA GGG GTA CCA GGC CTC CAG CCT GCT CGG GTG GCA GCT GTC Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val 305 310 315 320			960
50	TCC ACC CAC GTG GCC CTT GGG TCC TAT GCT CCT CTC ACA AGG CAT GGG Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly 325 330 335			1008
55	ACA CTT GTG GTG GAG GAT GTG GTG GCC TCC TGC TTT GCA GCT GTG GCT Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala 340 345 350			1056
60	GAC CAC CAT CTG GCT CAG TTG GCC TTC TGG CCC CTG CGA CTG TTT CCC Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro 355 360 365			1104
	AGT TTG GCA TGG GGC AGC TGG ACC CCA AGT GAG GGT GTT CAC TCC TAC Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr 370 375 380			1152
	CCT CAG ATG CTC TAC CGC CTG GGG CGT CTC TTG CTA GAA GAG AGC ACC Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr 385 390 395 400			1200
	TTC CAT CCA CTG GGC ATG TCT GGG GCA GGA AGC TGAAGGGACT CTAACCACTG Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser 405 410			1253

CCCTCCTGGA ACTGCTGTGC GTGGATCC

1281

5 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 10 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1314

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG	CTG	CTG	CTG	CTG	GCC	AGA	TGT	TTT	CTG	GTG	ATC	CTT	GCT	TCC	TCG	48	
Met	Leu	Leu	Leu	Leu	Ala	Arg	Cys	Phe	Leu	Val	Ile	Leu	Ala	Ser	Ser		
1	5							10					15				
25	CTG	CTG	GTG	TGC	CCC	GGG	CTG	GCC	TGT	GGG	CCC	GGC	AGG	GGG	TTT	GGA	96
	Leu	Leu	Val	Cys	Pro	Gly	Leu	Ala	Cys	Gly	Pro	Gly	Arg	Gly	Phe	Gly	
			20				25						30				
30	AAG	AGG	CGG	CAC	CCC	AAA	AAG	CTG	ACC	CCT	TTA	GCC	TAC	AAG	CAG	TTT	144
	Lys	Arg	Arg	His	Pro	Lys	Lys	Leu	Thr	Pro	Leu	Ala	Tyr	Lys	Gln	Phe	
			35				40					45					
35	ATT	CCC	AAC	GTA	GCC	GAG	AAG	ACC	CTA	GGG	GCC	AGC	GGC	AGA	TAT	GAA	192
	Ile	Pro	Asn	Val	Ala	Glu	Lys	Thr	Leu	Gly	Ala	Ser	Gly	Arg	Tyr	Glu	
			50				55					60					
40	GGG	AAG	ATC	ACA	AGA	AAC	TCC	GAA	CGA	TTT	AAG	GAA	CTC	ACC	CCC	AAT	240
	Gly	Lys	Ile	Thr	Arg	Asn	Ser	Glu	Arg	Phe	Lys	Glu	Leu	Thr	Pro	Asn	
			65				70			75		80					
45	TAC	AAC	CCC	GAC	ATC	ATA	TTT	AAG	GAT	GAG	GAA	AAC	ACG	GGA	GCA	GAC	288
	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	Glu	Asn	Thr	Gly	Ala	Asp	
			85				90			95							
50	CGG	CTG	ATG	ACT	CAG	AGG	TGC	AAA	GAC	AAG	TTA	AAT	GCC	TTG	GCC	ATC	336
	Arg	Leu	Met	Thr	Gln	Arg	Cys	Lys	Asp	Lys	Leu	Asn	Ala	Leu	Ala	Ile	
			100				105			110							
55	TCT	GTG	ATG	AAC	CAG	TGG	CCT	GGA	GTG	AGG	CTG	CGA	GTG	ACC	GAG	GGC	384
	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	
			115				120			125							
60	TGG	GAT	GAG	GAC	GGC	CAT	CAT	TCA	GAG	GAG	TCT	CTA	CAC	TAT	GAG	GGT	432
	Trp	Asp	Glu	Asp	Gly	His	His	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	
			130				135			140							
65	CGA	GCA	GTG	GAC	ATC	ACC	ACG	TCC	GAC	CGG	GAC	CGC	AGC	AAG	TAC	GGC	480
	Arg	Ala	Val	Asp	Ile	Thr	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	
			145				150			155		160					
70	ATG	CTG	GCT	CGC	CTG	GCT	GTG	GAA	GCA	GGT	TTC	GAC	TGG	GTC	TAC	TAT	528

	Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	
	165 170 175	
5	GAA TCC AAA GCT CAC ATC CAC TGT TCT GTG AAA GCA GAG AAC TCC GTG Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val	576
	180 185 190	
10	GCG GCC AAA TCC GGC GGC TGT TTC CCG GGA TCC GCC ACC GTG CAC CTG Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu	624
	195 200 205	
	GAG CAG GGC GGC ACC AAG CTG GTG AAG GAC TTA CGT CCC GGA GAC CGC Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg	672
15	210 215 220	
	GTG CTG GCG GCT GAC GAC CAG GGC CGG CTG CTG TAC AGC GAC TTC CTC Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu	720
	225 230 235 240	
20	ACC TTC CTG GAC CGC GAC GAA GGC GCC AAG AAG GTC TTC TAC GTG ATC Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile	768
	245 250 255	
25	GAG ACG CTG GAG CCG CGC GAG CGC CTG CTG CTC ACC GCC GCG CAC CTG Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu	816
	260 265 270	
30	CTC TTC GTG GCG CCG CAC AAC GAC TCG GGG CCC ACG CCC GGG CCA AGC Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser	864
	275 280 285	
	GCG CTC TTT GCC AGC CGC CTG CGC CCC GGG CAG CGC GTG TAC GTG GTG Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val	912
35	290 295 300	
	GCT GAA CGC GGC GGG GAC CGC CGG CTG CTG CCC GCC GCG GTG CAC AGC Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser	960
	305 310 315 320	
40	GTG ACG CTG CGA GAG GAG GAG GCG GGC GCG TAC GCG CCG CTC ACG GCG Val Thr Leu Arg Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala	1008
	325 330 335	
45	CAC GGC ACC ATT CTC ATC AAC CGG GTG CTC GCC TCG TGC TAC GCT GTC His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val	1056
	340 345 350	
50	ATC GAG GAG CAC AGC TGG GCA CAC CGG GCC TTC GCG CCT TTC CGC CTG Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu	1104
	355 360 365	
	GCG CAC GCG CTG CTG GCC GCG CTG GCA CCC GCC CGC ACG GAC GGC GGG Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly	1152
55	370 375 380	
	GGC GGG GGC AGC ATC CCT GCA GCG CAA TCT GCA ACG GAA GCG AGG GGC Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly	1200
	385 390 395 400	
60	GCG GAG CCG ACT GCG GGC ATC CAC TGG TAC TCG CAG CTG CTC TAC CAC Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His	1248
	405 410 415	

ATT GGC ACC TGG CTG TTG GAC AGC GAG ACC ATG CAT CCC TTG GGA ATG 1296
 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
 420 425 430

5 GCG GTC AAG TCC AGC TG 1313
 Ala Val Lys Ser Ser
 435

10 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

30 ATG CGG CTT TTG ACG AGA GTG CTG CTG GTG TCT CTT CTC ACT CTG TCC 48
 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
 1 5 10 15

35 TTG GTG GTG TCC GGA CTG GCC TGC GGT CCT GGC AGA GGC TAC GGC AGA 96
 Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
 20 25 30

40 AGA AGA CAT CCG AAG AAG CTG ACA CCT CTC GCC TAC AAG CAG TTC ATA 144
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45

45 CCT AAT GTC GCG GAG AAG ACC TTA GGG GCC AGC GGC AGA TAC GAG GGC 192
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60

50 AAG ATA ACG CGC AAT TCG GAG AGA TTT AAA GAA CTT ACT CCA AAT TAC 240
 Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80

55 AAT CCC GAC ATT ATC TTT AAG GAT GAG GAG AAC ACG GGA GCG GAC AGG 288
 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95

60 CTC ATG ACA CAG AGA TGC AAA GAC AAG CTG AAC TCG CTG GCC ATC TCT 336
 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
 100 105 110

65 GTA ATG AAC CAC TGG CCA GGG GTT AAG CTG CGT GTG ACA GAG GGC TGG 384
 Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125

70 GAT GAG GAC GGT CAC CAT TTT GAA GAA TCA CTC CAC TAC GAG GGA AGA 432
 Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg

	130	135	140	
5	GCT GTT GAT ATT ACC ACC TCT GAC CGA GAC AAG AGC AAA TAC GGG ACA Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr 145 150 155 160			480
10	CTG TCT CGC CTA GCT GTG GAG GCT GGA TTT GAC TGG GTC TAT TAC GAG Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu 165 170 175			528
15	TCC AAA GCC CAC ATT CAT TGC TCT GTC AAA GCA GAA AAT TCG GTT GCT Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala 180 185 190			576
20	GCG AAA TCT GGG GGC TGT TTC CCA GGT TCG GCT CTG GTC TCG CTC CAG Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln 195 200 205			624
25	GAC GGA GGA CAG AAG GCC GTG AAG GAC CTG AAC CCC GGA GAC AAG GTG Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val 210 215 220			672
30	CTG GCG GCA GAC AGC GCG GGA AAC CTG GTG TTC AGC GAC TTC ATC ATG Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met 225 230 235 240			720
35	TTC ACA GAC CGA GAC TCC ACG ACG CGA CGT GTG TTT TAC GTC ATA GAA Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu 245 250 255			768
40	ACG CAA GAA CCC GTT GAA AAG ATC ACC CTC ACC GCC GCT CAC CTC CTT Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu 260 265 270			816
45	TTT GTC CTC GAC AAC TCA ACG GAA GAT CTC CAC ACC ATG ACC GCC GCG Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala 275 280 285			864
50	TAT GCC AGC AGT GTC AGA GCC GGA CAA AAG GTG ATG GTT GTT GAT GAT Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp 290 295 300			912
55	AGC GGT CAG CTT AAA TCT GTC ATC GTG CAG CGG ATA TAC ACG GAG GAG Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu 305 310 315 320			960
60	CAG CGG GGC TCG TTC GCA CCA GTG ACT GCA CAT GGG ACC ATT GTG GTC Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val 325 330 335			1008
	GAC AGA ATA CTG GCG TCC TGT TAC GCC GTA ATA GAG GAC CAG GGG CTT Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu 340 345 350			1056
	GCG CAT TTG GCC TTC GCG CCC GCC AGG CTC TAT TAT TAC GTG TCA TCA Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Val Ser Ser 355 360 365			1104
	TTC CTG TCC CCC AAA ACT CCA GCA GTC GGT CCA ATG CGA CTT TAC AAC Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn 370 375 380			1152

	AGG AGG GGG TCC ACT GGT ACT CCA GGC TCC TGT CAT CAA ATG GGA ACG	1200
	Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr	
385	390	395
		400
5	TGG CTT TTG GAC AGC AAC ATG CTT CAT CCT TTG GGG ATG TCA GTA AAC	1248
	Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn	
	405	410
		415
10	TCA AGC TG	1256
	Ser Ser	

(2) INFORMATION FOR SEQ ID NO:6:

15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1425 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
25	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 1..1425	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	ATG CTG CTG CTG GCG AGA TGT CTG CTG CTA GTC CTC GTC TCC TCG CTG	48
	Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu	
	1 5 10 15	
35	CTG GTA TGC TCG GGA CTG GCG TGC GGA CCG GGC AGG GGG TTC GGG AAG	96
	Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys	
	20 25 30	
40	AGG AGG CAC CCC AAA AAG CTG ACC CCT TTA GCC TAC AAG CAG TTT ATC	144
	Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile	
	35 40 45	
45	CCC AAT GTG GCC GAG AAG ACC CTA GGC GCC AGC GGA AGG TAT GAA GGG	192
	Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly	
	50 55 60	
50	AAG ATC TCC AGA AAC TCC GAG CGA TTT AAG GAA CTC ACC CCC AAT TAC	240
	Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr	
	65 70 75 80	
	AAC CCC GAC ATC ATA TTT AAG GAT GAA GAA AAC ACC GGC GCG GAC AGG	288
	Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg	
	85 90 95	
55	CTG ATG ACT CAG AGG TGT AAG GAC AAG TTG AAC GCT TTG GCC ATC TCG	336
	Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser	
	100 105 110	
60	GTG ATG AAC CAG TGG CCA GGA GTG AAA CTG CGG GTG ACC GAG GGC TGG	384
	Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp	
	115 120 125	

	GAC GAA GAT GGC CAC CAC TCA GAG GAG TCT CTG CAC TAC GAG GGC CGC	432
	Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg	
	130 135 140	
5	GCA GTG GAC ATC ACC ACG TCT GAC CGC GAC CGC AGC AAG TAC GGC ATG	480
	Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met	
	145 150 155 160	
10	CTG GCC CGC CTG GCG GTG GAG GCC GGC TTC GAC TGG GTG TAC TAC GAG	528
	Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu	
	165 170 175	
15	TCC AAG GCA CAT ATC CAC TGC TCG GTG AAA GCA GAG AAC TCG GTG GCG	576
	Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala	
	180 185 190	
20	GCC AAA TCG GGA GGC TGC TTC CCG GGC TCG GCC ACG GTG CAC CTG GAG	624
	Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu	
	195 200 205	
	CAG GGC GGC ACC AAG CTG GTG AAG GAC CTG AGC CCC GGG GAC CGC GTG	672
	Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val	
	210 215 220	
25	CTG GCG GCG GAC GAC CAG GGC CGG CTG CTC TAC AGC GAC TTC CTC ACT	720
	Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr	
	225 230 235 240	
30	TTC CTG GAC CGC GAC GAC GGC GCC AAG AAG GTC TTC TAC GTG ATC GAG	768
	Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu	
	245 250 255	
35	ACG CGG GAG CCG CGC GAG CGC CTG CTG CTC ACC GCC GCG CAC CTG CTC	816
	Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu	
	260 265 270	
40	TTT GTG GCG CCG CAC AAC GAC TCG GCC ACC GGG GAG CCC GAG GCG TCC	864
	Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser	
	275 280 285	
	TCG GGC TCG GGG CCG CCT TCC GGG GGC GCA CTG GGG CCT CGG GCG CTG	912
	Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu	
	290 295 300	
45	TTC GCC AGC CGC GTG CGC CCG GGC CAG CGC GTG TAC GTG GTG GCC GAG	960
	Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu	
	305 310 315 320	
50	CGT GAC GGG GAC CGC CGG CTC CTG CCC GCC GCT GTG CAC AGC GTG ACC	1008
	Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr	
	325 330 335	
55	CTA AGC GAG GAG GCC GCG GGC GCC TAC GCG CCG CTC ACG GCC CAG GGC	1056
	Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly	
	340 345 350	
60	ACC ATT CTC ATC AAC CGG GTG CTG GCC TCG TGC TAC GCG GTC ATC GAG	1104
	Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu	
	355 360 365	
	GAG CAC AGC TGG GCG CAC CGG GCC TTC GCG CCC TTC CGC CTG GCG CAC	1152

	Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His	
	370 375 380	
5	GCG CTC CTG GCT GCA CTG GCG CCC GCG CGC ACG GAC CGC GGC GGG GAC	1200
	Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp	
	385 390 395 400	
10	AGC GGC GGC GGG GAC CGC GGG GGC GGC GGC AGA GTA GCC CTA ACC	1248
	Ser Gly Gly Asp Arg Gly Gly Gly Gly Arg Val Ala Leu Thr	
	405 410 415	
	GCT CCA GGT GCT GCC GAC GCT CCG GGT GCG GGG GCC ACC GCG GGC ATC	1296
	Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile	
	420 425 430	
15	CAC TGG TAC TCG CAG CTG CTC TAC CAA ATA GGC ACC TGG CTC CTG GAC	1344
	His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp	
	435 440 445	
20	AGC GAG GCC CTG CAC CCG CTG GGC ATG GCG GTC AAG TCC AGC NNN AGC	1392
	Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser	
	450 455 460	
25	CGG GGG GCC GGG GGA GGG GCG CGG GAG GGG GCC	1425
	Arg Gly Ala Gly Gly Ala Arg Glu Gly Ala	
	465 470 475	

30 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- 40 (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 51..1283

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	CATCAGCCCCA CCAGGAGACC TCGCCCGCCG CTCCCCGGGG CTCCCCGGCC ATG TCT	56
50	Met Ser	
	1	
	CCC GCC CGG CTC CGG CCC CGA CTG CAC TTC TGC CTG GTC CTG TTG CTG	104
	Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu Leu Leu	
	5 10 15	
55	CTG CTG GTG GTG CCC GCG GCA TGG GGC TGC GGG CCG GGT CGG GTG GTG	152
	Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg Val Val	
	20 25 30	
60	GGC AGC CGC CGG CGA CCG CCA CGC AAA CTC GTG CCG CTC GCC TAC AAG	200
	Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala Tyr Lys	
	35 40 45 50	

	CAG TTC AGC CCC AAT GTG CCC GAG AAG ACC CTG GGC GCC AGC GGA CGC Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser Gly Arg 55 60 65	248
5	TAT GAA GGC AAG ATC GCT CGC AGC TCC GAG CGC TTC AAG GAG GTC ACC Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu Leu Thr 70 75 80	296
10	CCC AAT TAC AAT CCA GAC ATC ATC TTC AAG GAC GAG GAG AAC ACA GGC Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly 85 90 95	344
15	GCC GAC CGC CTC ATG ACC CAG CGC TGC AAG GAC CGC CTG AAC TCG CTG Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn Ser Leu 100 105 110	392
20	GCT ATC TCG GTG ATG AAC CAG TGG CCC GGT GTG AAG CTG CGG GTG ACC Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr 115 120 125 130	440
25	GAG GGC TGG GAC GAG GAC GGC CAC CAC TCA GAG GAG TCC CTG CAT TAT Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr 135 140 145	488
30	GAG GGC CGC GCG GTG GAC ATC ACC ACA TCA GAC CGC GAC CGC AAT AAG Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys 150 155 160	536
35	TAT GGA CTG CTG CGC TTG GCA GTG GAG GCC GGC TTT GAC TGG GTG Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165 170 175	584
40	TAT TAC GAG TCA AAG GCC CAC GTG CAT TGC TCC GTC AAG TCC GAG CAC Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His 180 185 190	632
45	TCG GCC GCA GCC AAG ACG GGC GGC TGC TTC CCT GCC GGA GCC CAG GTA Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val 195 200 205 210	680
50	CGC CTG GAG AGT GGG GCG CGT GTG GCC TTG TCA GCC GTG AGG CCG GGA Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly 215 220 225	728
55	GAC CGT GTG CTG GCC ATG GGG GAG GAT GGG AGC CCC ACC TTC AGC GAT Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp 230 235 240	776
60	GTG CTC ATT TTC CTG GAC CGC GAG CCC CAC AGG CTG AGA GCC TTC CAG Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln 245 250 255	824
65	GTC ATC GAG ACT CAG GAC CCC CCA CGC CGC CTG GCA CTC ACA CCC GCT Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala 260 265 270	872
70	CAC CTG CTC TTT ACG GCT GAC AAT CAC ACG GAG CCG GCA GCC CGC TTC His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe 275 280 285 290	920
75	CGG GCC ACA TTT GCC AGC CAC GTG CAG CCT GGC CAG TAC GTG CTG GTG 295	968

	Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val	
	295 300 305	
5	GCT GGG GTG CCA GGC CTG CAG CCT GCC CGC GTG GCA GCT GTC TCT ACA	1016
	Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr	
	310 315 320	
10	CAC GTG GCC CTC GGG GCC TAC GCC CCG CTC ACA AAG CAT GGG ACA CTG	1064
	His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu	
	325 330 335	
15	GTC GTG GAG GAT GTG GTG GCA TCC TGC TTC GCG GCC GTG GCT GAC CAC	1112
	Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His	
	340 345 350	
20	CAC CTG GCT CAG TTG GCC TTC TGG CCC CTG AGA CTC TTT CAC AGC TTG	1160
	His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu	
	355 360 365 370	
25	GCA TGG GGC AGC TGG ACC CCG GGG GAG GGT GTG CAT TGG TAC CCC CAG	1208
	Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln	
	375 380 385	
30	CTG CTC TAC CGC CTG GGG CGT CTC CTG CTA GAA GAG GGC AGC TTC CAC	1256
	Leu Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Gly Ser Phe His	
	390 395 400	
	CCA CTG GGC ATG TCC GGG GCA GGG AGC TGAAAGGACT CCACCGCTGC	1303
	Pro Leu Gly Met Ser Gly Ala Gly Ser	
	405 410	
	CCTCCTGGAA CTGCTGTACT GGGTCCAGAA GCCTCTCAGC CAGGAGGGAG CTGGCCCTGG	1363
35	AAGGGACCTG AGCTGGGGGA CACTGGCTCC TGCCATCTCC TCTGCCATGA AGATACACCA	1423
	TTGAGACTTG ACTGGGCAAC ACCAGCGTCC CCCACCCGCG TCGTGGTGTGTA GTCATAGAGC	1483
	TGCAAGCTGA GCTGGCGAGG GGATGGTTGT TGACCCCTCT CTCCTAGAGA CCTTGAGGCT	1543
40	GGCACGGCGA CTCCCAACTC AGCCTGCTCT CACTACGAGT TTTCATACTC TGCCTCCCCC	1603
	ATTGGGAGGG CCCATTCCC	1622
45	(2) INFORMATION FOR SEQ ID NO:8:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1191 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: both	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
55	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 1..1191	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	

ATG GCT CTC CTG ACC AAT CTA CTG CCC TTG TGC TGC TTG GCA CTT CTG

	Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu	
	1 5 10 15	
5	GCG CTG CCA GCC CAG AGC TGC GGG CCG GGC CGG GGG CCG GTT GGC CGG Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg	96
	20 25 30	
10	CGC CGC TAT GCG CGC AAG CAG CTC GTG CCG CTA CTC TAC AAG CAA TTT Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe	144
	35 40 45	
15	GTG CCC GGC GTG CCA GAG CGG ACC CTG GGC GCC AGT GGG CCA GCG GAG Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu	192
	50 55 60	
20	GGG AGG GTG GCA AGG GGC TCC GAG CGC TTC CCG GAC CTC GTG CCC AAC Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn	240
	65 70 75 80	
25	TAC AAC CCC GAC ATC ATC TTC AAG GAT GAG GAG AAC AGT GGA GCC GAC Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp	288
	85 90 95	
30	CGC CTG ATG ACC GAG CGT TGC AAG GAG AGG GTG AAC GCT TTG GCC ATT Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile	336
	100 105 110	
35	GCC GTG ATG AAC ATG TGG CCC GGA GTG CGC CTA CGA GTG ACT GAG GGC Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly	384
	115 120 125	
40	TGG GAC GAG GAC GGC CAC CAC GCT CAG GAT TCA CTC CAC TAC GAA GGC Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly	432
	130 135 140	
45	CGT GCT TTG GAC ATC ACT ACG TCT GAC CGC GAC CGC AAC AAG TAT GGG Arg Ala Leu Asp Ile Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly	480
	145 150 155 160	
50	TTG CTG GCG CGC CTC GCA GTG GAA GCC GGC TTC GAC TGG GTC TAC TAC Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr	528
	165 170 175	
55	GAG TCC CGC AAC CAC GTC CAC GTG TCG GTC AAA GCT GAT AAC TCA CTG Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu	576
	180 185 190	
60	GGC GTC CGG GCG GGC GGC TGC TTT CCG GGA AAT GCA ACT GTG CGC CTG Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu	624
	195 200 205	
65	TGG AGC GGC GAG CGG AAA GGG CTG CGG GAA CTG CAC CGC GGA GAC TGG Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp	672
	210 215 220	
70	GTT TTG GCG GCC GAT GCG TCA GGC CGG GTG GTG CCC ACG CCG GTG CTG Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu	720
	225 230 235 240	
75	CTC TTC CTG GAC CGG GAC TTG CAG CGC CGG GCT TCA TTT GTG GCT GTG Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val	768
	245 250 255	

GAG ACC GAG TGG CCT CCA CGC AAA CTG TTG CTC ACG CCC TGG CAC CTG 816
 Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270

5 GTG TTT GCC GCT CGA GGG CCG GCG CCC GCG CCA GGC GAC TTT GCA CCG 864
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285

10 GTG TTC GCG CGC CGG CTA CGC GCT GGG GAC TCG GTG CTG GCG CCC GGC 912
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

15 GGG GAT GCG CTT CGG CCA GCG CGC GTG GCC CGT GTG GCG CGG GAG GAA 960
 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320

20 GCC GTG GGC GTG TTC GCG CCG CTC ACC GCG CAC GGG ACG CTG CTG GTG 1008
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

25 AAC GAT GTC CTG GCC TCT TGC TAC GCG GTT CTG GAG AGT CAC CAG TGG 1056
 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

GCG CAC CGC GCT TTT GCC CCC TTG AGA CTG CTG CAC GCG CTA GGG GCG 1104
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

30 CTG CTC CCC GGC GGG GCC GTC CAG CCG ACT GGC ATG CAT TGG TAC TCT 1152
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

35 CGG CTC CTC TAC CGC TTA GCG GAG GAG CTA CTG GGC TG 1191
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

40 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1248

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GAC GTA AGG CTG CAT CTG AAG CAA TTT GCT TTA CTG TGT TTT ATC 48
 Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 60 1 5 10 15

AGC TTG CTT CTG ACG CCT TGT GGA TTA GCC TGT GGT CCT GGT AGA GGT 96

	Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly	
	20 25 30	
5	TAT GGA AAA CGA AGA CAC CCA AAG AAA TTA ACC CCG TTG GCT TAC AAG Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys 35 40 45	144
10	CAA TTC ATC CCC AAC GTT GCT GAG AAA ACG CTT GGA GCC AGC GGC AAA Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys 50 55 60	192
15	TAC GAA GGC AAA ATC ACA AGG AAT TCA GAG AGA TTT AAA GAG CTG ATT Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile 65 70 75 80	240
20	CCG AAT TAT AAT CCC GAT ATC ATC TTT AAG GAC GAG GAA AAC ACA AAC Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn 85 90 95	288
25	GCT GAC AGG CTG ATG ACC AAG CGC TGT AAG GAC AAG TTA AAT TCG TTG Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu 100 105 110	336
30	GCC ATA TCC GTC ATG AAC CAC TGG CCC GGC GTG AAA CTG CGC GTC ACT Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr 115 120 125	384
35	GAA GGC TGG GAT GAG GAT GGT CAC CAT TTA GAA GAA TCT TTG CAC TAT Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr 130 135 140	432
40	GAG GGA CGG GCA GTG GAC ATC ACT ACC TCA GAC AGG GAT AAA AGC AAG Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys 145 150 155 160	480
45	TAT GGG ATG CTA TCC AGG CTT GCA GTG GAG GCA GGA TTC GAC TGG GTC Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val 165 170 175	528
50	TAT TAT GAA TCT AAA GCC CAC ATA CAC TGC TCT GTC AAA GCA GAA AAT Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn 180 185 190	576
55	TCA GTG GCT GCT AAA TCA GGA GGA TGT TTT CCT GGG TCT GGG ACG GTG Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val 195 200 205	624
60	ACA CTT GGT GAT GGG ACG AGG AAA CCC ATC AAA GAT CTT AAA GTG GGC Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly 210 215 220	672
	GAC CGG GTT TTG GCT GCA GAC GAG AAG GGA AAT GTC TTA ATA AGC GAC Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp 225 230 235 240	720
	TTT ATT ATG TTT ATA GAC CAC GAT CCG ACA ACG AGA AGG CAA TTC ATC Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile 245 250 255	768
	GTC ATC GAG ACG TCA GAA CCT TTC ACC AAG CTC ACC CTC ACT GCC GCG Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala 260 265 270	816

	CAC CTA GTT TTC GTT GGA AAC TCT TCA GCA GCT TCG GGT ATA ACA GCA	864
	His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala	
	275 280 285	
5	ACA TTT GCC AGC AAC GTG AAG CCT GGA GAT ACA GTT TTA GTG TGG GAA	912
	Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu	
	290 295 300	
10	GAC ACA TGC GAG AGC CTC AAG AGC GTT ACA GTG AAA AGG ATT TAC ACT	960
	Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr	
	305 310 315 320	
15	GAG GAG CAC GAG GGC TCT TTT GCG CCA GTC ACC GCG CAC GGA ACC ATA	1008
	Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile	
	325 330 335	
20	ATA GTG GAT CAG GTG TTG GCA TCG TGC TAC GCG GTC ATT GAG AAC CAC	1056
	Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His	
	340 345 350	
	AAA TGG GCA CAT TGG GCT TTT GCG CCG GTC AGG TTG TGT CAC AAG CTG	1104
	Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu	
25	355 360 365	
	ATG ACG TGG CTT TTT CCG GCT CGT GAA TCA AAC GTC AAT TTT CAG GAG	1152
	Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu	
	370 375 380	
30	GAT GGT ATC CAC TGG TAC TCA AAT ATG CTG TTT CAC ATC GGC TCT TGG	1200
	Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp	
	385 390 395 400	
35	CTG CTG GAC AGA GAC TCT TTC CAT CCA CTC GGG ATT TTA CAC TTA AGT	1248
	Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser	
	405 410 415	
	TGA	1251
40	(2) INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 425 amino acids	
45	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile	
	1 5 10 15	
55	Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly	
	20 25 30	
60	Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys	
	35 40 45	
	Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg	

	50	55	60	
	Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr			
5	65	70	75	80
	Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly			
	85		90	95
10	Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu			
	100	105		110
	Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr			
	115	120		125
15	Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr			
	130	135		140
20	Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys			
	145	150	155	160
	Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val			
	165	170		175
25	Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn			
	180	185		190
	Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val			
	195	200		205
30	His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly			
	210	215		220
	Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp			
35	225	230	235	240
	Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr			
	245	250		255
40	Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala			
	260	265		270
	His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly			
	275	280		285
45	Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln			
	290	295		300
	Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser			
50	305	310	315	320
	Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro			
	325	330		335
55	Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys			
	340	345		350
	Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro			
	355	360		365
60	Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala			
	370	375		380

10 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
385 390 395 400

5 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
405 410 415

Pro Leu Gly Met Val Ala Pro Ala Ser
420 425

10

(2) INFORMATION FOR SEQ ID NO:11:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15

Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30

30 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45

35 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60

Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65 70 75 80

40 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Asn Ser Gly Ala Asp
85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110

45 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

50 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145 150 155 160

55 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175

Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
180 185 190

60 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
195 200 205

Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220
 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
 5 225 230 235 240
 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255
 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 10 260 265 270
 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 15 275 280 285
 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300
 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 20 305 310 315 320
 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335
 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 25 340 345 350
 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365
 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 30 370 375 380
 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
 35 385 390 395

(2) INFORMATION FOR SEQ ID NO:12:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
 1 5 10 15

Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
 55 20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 60 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

5 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

10 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

15 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

20 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190

25 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220

30 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
 225 230 235 240

35 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
 245 250 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270

40 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285

His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300

45 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320

50 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350

55 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380

60 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr
 385 390 395 400

Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
405 410

5

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 437 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
1 5 10 15

Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
20 25 30

25 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
35 40 45

30 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
50 55 60

Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
65 70 75 80

35 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
85 90 95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
100 105 110

40 Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

45 Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
130 135 140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
145 150 155 160

50 Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175

Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
180 185 190

55 Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
195 200 205

60 Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
210 215 220

Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu

225	230	235	240
Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile			
	245	250	255
5	Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu		
	260	265	270
10	Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser		
	275	280	285
Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val			
	290	295	300
15	Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser		
	305	310	315
Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala			
	325	330	335
20	His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val		
	340	345	350
25	Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu		
	355	360	365
Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly			
	370	375	380
30	Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly		
	385	390	395
Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His			
	405	410	415
35	Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met		
	420	425	430
40	Ala Val Lys Ser Ser		
	435		

(2) INFORMATION FOR SEQ ID NO:14:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15
60 Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30
Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile

	35	40	45
	Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly		
5	50 55 60		
	Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr		
	65 70 75 80		
10	Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg		
	85 90 95		
	Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser		
	100 105 110		
15	Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp		
	115 120 125		
	Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg		
20	130 135 140		
	Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr		
	145 150 155 160		
25	Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu		
	165 170 175		
	Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala		
	180 185 190		
30	Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln		
	195 200 205		
	Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val		
35	210 215 220		
	Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met		
	225 230 235 240		
40	Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu		
	245 250 255		
	Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu		
	260 265 270		
45	Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala		
	275 280 285		
	Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp		
50	290 295 300		
	Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu		
	305 310 315 320		
55	Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val		
	325 330 335		
	Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu		
	340 345 350		
60	Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Val Ser Ser		
	355 360 365		

Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
370 375 380

5 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
405 410 415

10 Ser Ser

15 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
1 5 10 15

30 Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

35 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

40 Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

45 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
100 105 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

50 Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

55 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
145 150 155 160

Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

60 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
 195 200 205

5 Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
 210 215 220

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
 225 230 235 240

10 Phe Leu Asp Arg Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
 245 250 255

Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
 260 265 270

15 Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
 275 280 285

20 Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300

Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320

25 Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350

30 Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365

35 Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400

40 Ser Gly Gly Asp Arg Gly Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430

45 His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445

50 Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460

Arg Gly Ala Gly Gly Gly Ala Arg Glu Gly Ala
 465 470 475

55 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
20 25 30

10 Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

15 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
20 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

25 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

30 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
35 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180 185 190

40 Glu His Ser Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
195 200 205

Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
210 215 220

45 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
225 230 235 240

Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
50 245 250 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
260 265 270

55 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
275 280 285

Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
290 295 300

60 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
305 310 315 320

Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
 325 330 335
 5 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
 355 360 365
 10 Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
 370 375 380
 15 Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Gly Ser
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410
 20 (2) INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 30 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 35 20 25 30
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45
 40 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80
 45 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95
 50 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125
 55 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140
 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160
 60 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175

Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190

5 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205

Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220

10 Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240

15 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255

Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270

20 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

25 Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320

30 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

35 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

40 Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

45 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 416 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

60 Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
 20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

5 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
 65 70 75 80

10 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
 85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
 100 105 110

15 Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

20 Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
 145 150 155 160

25 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190

30 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205

35 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220

Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240

40 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255

Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270

45 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285

50 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300

Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320

55 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335

Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350

60 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365

Met	Thr	Trp	Leu	Phe	Pro	Ala	Arg	Glu	Ser	Asn	Val	Asn	Phe	Gln	Glu
370						375					380				

5	Asp	Gly	Ile	His	Trp	Tyr	Ser	Asn	Met	Leu	Phe	His	Ile	Gly	Ser	Trp
385						390					395				400	

Leu	Leu	Asp	Arg	Asp	Ser	Phe	His	Pro	Leu	Gly	Ile	Leu	His	Leu	Ser
						405				410				415	

10

(2) INFORMATION FOR SEQ ID NO:19:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

30	ATG	GAT	AAC	CAC	AGC	TCA	G TG	CCT	TGG	GCC	AGT	GCC	GCC	AGT	GTC	ACC	48
	Met	Asp	Asn	His	Ser	Ser	Val	Pro	Trp	Ala	Ser	Ala	Ala	Ser	Val	Thr	
	1				5					10					15		

35	TGT	CTC	TCC	CTG	GGA	TGC	CAA	ATG	CCA	CAG	TTC	CAG	TTC	CAG	TTC	CAG	96
	Cys	Leu	Ser	Leu	Gly	Cys	Gln	Met	Pro	Gln	Phe	Gln	Phe	Gln	Phe	Gln	
					20				25					30			

40	CTC	CAA	ATC	CGC	AGC	GAG	CTC	CAT	CTC	CGC	AAG	CCC	GCA	AGA	AGA	ACG	144
	Leu	Gln	Ile	Arg	Ser	Glu	Leu	His	Leu	Arg	Lys	Pro	Ala	Arg	Arg	Thr	
					35				40					45			

45	CAA	ACG	ATG	CGC	CAC	ATT	GCG	CAT	ACG	CAG	CGT	TGC	CTC	AGC	AGG	CTG	192
	Gln	Thr	Met	Arg	His	Ile	Ala	His	Thr	Gln	Arg	Cys	Leu	Ser	Arg	Leu	
					50				55			60					

50	ACC	TCT	CTG	GTG	GCC	CTG	CTG	ATC	GTC	TTG	CCG	ATG	GTC	TTT	AGC	240
	Thr	Ser	Leu	Val	Ala	Leu	Leu	Ile	Val	Leu	Pro	Met	Val	Phe	Ser	
					65			70		75			80			

55	CCG	GCT	CAC	AGC	TGC	GGT	CCT	GGC	CGA	GGA	TTG	GGT	CGT	CAT	AGG	GCG	288
	Pro	Ala	His	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Leu	Gly	Arg	His	Arg	Ala	
					85			90			95						

60	CGC	AAC	CTG	TAT	CCG	CTG	GTC	CTC	AAG	CAG	ACA	ATT	CCC	AAT	CTA	TCC	336
	Arg	Asn	Leu	Tyr	Pro	Leu	Val	Leu	Lys	Gln	Thr	Ile	Pro	Asn	Leu	Ser	
					100			105			110						

65	GAG	TAC	ACG	AAC	AGC	GCC	TCC	GGA	CCT	CTG	GAG	GGT	GTG	ATC	CGT	CGG	384
	Glu	Tyr	Thr	Asn	Ser	Ala	Ser	Gly	Pro	Leu	Glu	Gly	Val	Ile	Arg	Arg	
					115			120			125						

70	GAT	TCG	CCC	AAA	TTC	AAG	GAC	CTC	GTG	CCC	AAC	TAC	AAC	AGG	GAC	ATC	432
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	Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile		
	130 135 140		
5	CTT TTC CGT GAC GAG GAA GGC ACC GGA GCG GAT GGC TTG ATG AGC AAG Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys 145 150 155 160		480
10	CGC TGC AAG GAG AAG CTA AAC GTG CTG GCC TAC TCG GTG ATG AAC GAA Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu 165 170 175		528
	TGG CCC GGC ATC CGG CTG CTG GTC ACC GAG AGC TGG GAC GAG GAC TAC Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr 180 185 190		576
15	CAT CAC GGC CAG GAG TCG CTC CAC TAC GAG GGC CGA GCG GTG ACC ATT His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile 195 200 205		624
20	GCC ACC TCC GAT CGC GAC CAG TCC AAA TAC GGC ATG CTC GCT CGC CTG Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu 210 215 220		672
25	GCC GTC GAG GCT GGA TTC GAT TGG GTC TCC TAC GTC AGC AGG CGC CAC Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His 225 230 235 240		720
30	ATC TAC TGC TCC GTC AAG TCA GAT TCG TCG ATC AGT TCC CAC GTG CAC Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His 245 250 255		768
	GGC TGC TTC ACG CCG GAG AGC ACA GCG CTG CTG GAG AGT GGA GTC CGG Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg 260 265 270		816
35	AAG CCG CTC GGC GAG CTC TCT ATC GGA GAT CGT GTT TTG AGC ATG ACC Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr 275 280 285		864
40	GCC AAC GGA CAG GCC GTC TAC AGC GAA GTG ATC CTC TTC ATG GAC CGC Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg 290 295 300		912
45	AAC CTC GAG CAG ATG CAA AAC TTT GTG CAG CTG CAC ACG GAC GGT GGA Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly 305 310 315 320		960
50	GCA GTG CTC ACG GTG ACG CCG GCT CAC CTG GTT AGC GTT TGG CAG CCG Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro 325 330 335		1008
	GAG AGC CAG AAG CTC ACG TTT GTG TTT GCG CAT CGC ATC GAG GAG AAG Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys 340 345 350		1056
55	AAC CAG GTG CTC GTA CGG GAT GTG GAG ACG GGC GAG CTG AGG CCC CAG Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln 355 360 365		1104
60	CGA GTG GTC AAG TTG GGC AGT GTG CGC AGT AAG GGC GTG GTC GCG CCG Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro 370 375 380		1152

CTG ACC CGC GAG GGC ACC ATT GTG GTC AAC TCG GTG GCC GCC AGT TGC 1200
 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400
 5 TAT GCG GTG ATC AAC AGT CAG TCG CTG GCC CAC TGG GGA CTG GCT CCC 1248
 Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415
 10 ATG CGC CTG CTG TCC ACG CTG GAG GCG TGG CTG CCC GCC AAG GAG CAG 1296
 Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430
 15 TTG CAC AGT TCG CCG AAG GTG GTG AGC TCG GCG CAG CAG CAG AAT GGC 1344
 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445
 20 ATC CAT TGG TAT GCC AAT GCG CTC TAC AAG GTC AAG GAC TAC GTG CTG 1392
 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460
 25 CCG CAG AGC TGG CGC CAC GAT TGA 1416
 Pro Gln Ser Trp Arg His Asp
 465 470
 (2) INFORMATION FOR SEQ ID NO:20:
 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
 40 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15
 45 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
 20 25 30
 50 Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
 35 40 45
 55 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
 50 55 60
 60 Thr Ser Leu Val Ala Leu Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65 70 75 80
 65 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
 85 90 95
 70 Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
 100 105 110
 75 Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
 115 120 125
 80 Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile

	130	135	140	
	Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys			
	145	150	155	160
5	Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu			
	165	170	175	
	Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr			
10	180	185	190	
	His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile			
	195	200	205	
15	Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu			
	210	215	220	
	Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His			
20	225	230	235	240
	Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His			
	245	250	255	
25	Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg			
	260	265	270	
	Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr			
	275	280	285	
30	Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg			
	290	295	300	
	Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly			
35	305	310	315	320
	Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro			
	325	330	335	
40	Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys			
	340	345	350	
	Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln			
	355	360	365	
45	Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro			
	370	375	380	
	Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys			
50	385	390	395	400
	Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro			
	405	410	415	
55	Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln			
	420	425	430	
	Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly			
	435	440	445	
60	Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu			
	450	455	460	

Pro Gln Ser Trp Arg His Asp
465 470

5 (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide
(v) FRAGMENT TYPE: internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

20 Cys Gly Pro Gly Arg Gly Xaa Gly Arg Arg His Pro Lys Lys Leu
1 5 10 15

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

25 Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

30 Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
50 55 60

35 Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

40 Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

45 Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
100 105 110

50 Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
115 120 125

55 Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
130 135 140

60 Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
145 150 155 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe
165 170 175

Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
180 185 190

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
195 200 205

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
210 215 220

(2) INFORMATION FOR SEQ ID NO:22:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

10 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

15 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
1 5 10 15

20 Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
20 25 30

20 Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
35 40 45

25 Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
50 55 60

30 Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
65 70 75 80

35 Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
85 90 95

35 Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
100 105 110

40 His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
115 120 125

40 Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
130 135 140

45 Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
145 150 155 160

45 His Xaa Ser Val Lys Xaa Xaa
165

We claim:

1. A method for promoting survival of substantia nigra neuronal cells comprising
5 contacting the cells with a trophic amount of a *ptc* therapeutic.
2. A method for promoting survival of dopaminergic cells comprising contacting the
cells with a trophic amount of a *ptc* therapeutic.
- 10 3. A method for promoting survival of GABA-nergic cells comprising contacting the
cells with a trophic amount of a *ptc* therapeutic.
4. A method for treating a disorder characterized by loss of dopaminergic and/or
15 GABA-nergic neurons which comprises administering to a patient in need thereof
a therapeutically effective amount of a *ptc* therapeutic.
5. A method for treating or preventing Parkinson's disease comprising administering
to a patient in need thereof a therapeutically effective amount of a *ptc* therapeutic.
- 20 6. A method for treating or preventing Huntington's disease comprising
administering to a patient in need thereof a therapeutically effective amount of a
ptc therapeutic.
7. The method of any of claims 1-6, wherein the *ptc* therapeutic binds to *patched*
25 and mimics *hedgehog*-mediated *patched* signal transduction.
8. The method of claim 7, wherein the *ptc* therapeutic is a small organic molecule.
9. The method of claim 7, wherein the binding of the *ptc* therapeutic to *patched*
30 results in upregulation of *patched* and/or *gli* expression.

10. The method of any of claims 1-6, wherein the *ptc* therapeutic is a small organic molecule which interacts with neuronal cells to mimic *hedgehog*-mediated *patched* signal transduction.
- 5 11. The method of any of claims 1-6, wherein the *ptc* therapeutic mimics *hedgehog*-mediated *patched* signal transduction by altering the localization, protein-protein binding and/or enzymatic activity of an intracellular protein involved in a *patched* signal pathway.
- 10 12. The method of any of claims 1-6, wherein the *ptc* therapeutic alters the level of expression of a *hedgehog* protein, a *patched* protein or a protein involved in the intracellular signal transduction pathway of *patched*.
- 15 13. The method of claim 12, wherein the *ptc* therapeutic is an antisense construct which inhibits the expression of a protein which is involved in the signal transduction pathway of *patched* and the expression of which antagonizes *hedgehog*-mediated signals.
- 20 14. The method of claim 13, wherein the antisense construct is an oligonucleotide of about 20-30 nucleotides in length and has a GC content of at least 50 percent.
- 15 15. The method of claim 14, wherein the antisense oligonucleotide is selected from the group consisting of:

5'-GTCCTGGCGCCGCCGCCGCCGCGCC;

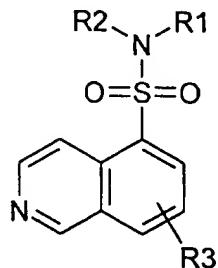
5'-TTCCGATGACCGGCCTTCGCGGTGA; and

5'-GTGACGGAAAGGTGCAGGCCACACT
- 25 16. The method of claim 12, wherein the *ptc* therapeutic is a small organic molecule which binds to *patched* and regulates *patched*-dependent gene expression.

17. The method of claim 11, wherein the *ptc* therapeutic is an inhibitor of protein kinase A.

18. The method of claim 17, wherein the PKA inhibitor is a 5-isoquinolinesulfonamide.

19. The method of claim 18, wherein the PKA inhibitor is represented in the general formula:



10 wherein,

R₁ and R₂ each can independently represent hydrogen, and as valence and stability permit a lower alkyl, a lower alkenyl, a lower alkynyl, a carbonyl (such as a carboxyl, an ester, a formate, or a ketone), a thiocarbonyl (such as a thioester, a thioacetate, or a thioformate), an amino, an acylamino, an amido, a cyano, a nitro, an azido, a sulfate, a sulfonate, a sulfonamido, -(CH₂)_m-R₈, -(CH₂)_m-OH, -(CH₂)_m-O-lower alkyl, -(CH₂)_m-O-lower alkenyl, -(CH₂)_n-O-(CH₂)_m-R₈, -(CH₂)_m-SH, -(CH₂)_m-S-lower alkyl, -(CH₂)_m-S-lower alkenyl, -(CH₂)_n-S-(CH₂)_m-R₈, or

R₁ and R₂ taken together with N form a heterocycle (substituted or unsubstituted);

20 R₃ is absent or represents one or more substitutions to the isoquinoline ring such as a lower alkyl, a lower alkenyl, a lower alkynyl, a carbonyl (such as a carboxyl, an ester, a formate, or a ketone), a thiocarbonyl (such as a thioester, a thioacetate, or a thioformate), an amino, an acylamino, an amido, a cyano, a nitro, an azido, a sulfate, a sulfonate, a sulfonamido, -(CH₂)_m-R₈, -(CH₂)_m-OH, -(CH₂)_m-O-lower alkyl, -(CH₂)_m-

O-lower alkenyl, -(CH₂)_n-O-(CH₂)_m-R₈, -(CH₂)_m-SH, -(CH₂)_m-S-lower alkyl, -(CH₂)_m-S-lower alkenyl, -(CH₂)_n-S-(CH₂)_m-R₈;

R₈ represents a substituted or unsubstituted aryl, aralkyl, cycloalkyl, cycloalkenyl, or heterocycle; and

5 n and m are independently for each occurrence zero or an integer in the range of 1 to 6.

20. The method of claim 17, wherein the PKA inhibitor is a cyclic AMP analog.
- 10 21. The method of claim 17, wherein the PKA inhibitor is selected from the group consisting of N-[2-((p-bromocinnamyl)amino)ethyl]-5-isoquinolinesulfonamide, 1-(5-isoquinoline-sulfonyl)-2-methylpiperazine, KT5720, 8-bromo-cAMP, dibutyryl-cAMP and PKA Heat Stable Inhibitor isoform α .
- 15 22. The method of any of claims 4-6, wherein a patient is being treated prophylactically.
- 20 23. A therapeutic preparation of a small molecule antagonist of *patched*, which *patched* antagonist is provided in a pharmaceutically acceptable carrier and in an amount sufficient to promote survival of dopaminergic cells in a mammal.
24. A therapeutic preparation of a small molecule antagonist of *patched*, which *patched* antagonist is provided in a pharmaceutically acceptable carrier and in an amount sufficient to promote survival of dopaminergic cells in an adult human.
- 25 25. The preparation of claim 24, which *patched* antagonist binds to *patched*.

26. The preparation of claim 24, wherein the *patched* antagonist is provided in an amount sufficient to promote survival of dopaminergic cells in a mammal treated with MPTP at 1mg/kg.
- 5 27. The preparation of claim 24, wherein the *patched* antagonist is provided in an amount sufficient to promote survival of dopaminergic cells in a mammal treated with MPTP at 10mg/kg.
- 10 28. A method for limiting damage to neuronal cells by Parkinsonian conditions, comprising administering to a patient a gene activation construct which recombines with a genomic *hedgehog* gene of the patient to provide a heterologous transcriptional regulatory sequence operatively linked to a coding sequence of the *hedgehog* gene.
- 15 29. An isolated and/or recombinantly produced polypeptide comprising an amino acid sequence which is at least 95 percent identical to a sequence represented by SEQ ID. NO. 16 or 17, or a bioactive extracellular fragment thereof.
- 20 30. An isolated and/or recombinantly produced polypeptide encoded by a nucleic acid which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID. NO. 16 and SEQ ID. NO. 17.
- 25 31. An isolated and/or recombinantly produced *Dhh* hedgehog polypeptide, or a bioactive extracellular fragment thereof, encoded by a human *Dhh* gene.
32. An isolated and/or recombinantly produced *Ihh* hedgehog polypeptide, or a bioactive extracellular fragment thereof, encoded by a human *Ihh* gene.
- 30 33. The polypeptide of any of claims 29-32, formulated in a pharmaceutically acceptable carrier.

34. The polypeptide of any of claims 29-32, wherein the polypeptide is purified to at least 80% by dry weight.
- 5 35. An isolated nucleic acid encoding a polypeptide comprising a *hedgehog* amino acid sequence which is at least 95 percent identical to a *hedgehog* protein selected from the group consisting of SEQ ID No:16 and SEQ ID No:17, and fragments thereof, which *hedgehog* amino acid sequence (i) binds to a *patched* protein, (ii) regulates differentiation of neuronal cells, (iii) regulates survival of differentiated neuronal cells, (iv) regulates proliferation of chondrocytes, (v) regulates proliferation of testicular germ line cells, or (vi) functionally replaces *Drosophila Hedgehog* in a transgenic *Drosophila* fly, or a combination thereof.
- 10 36. An isolated nucleic acid encoding a polypeptide having a *hedgehog* amino acid sequence encoded by a nucleic acid which hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID No:7 and SEQ ID No:8, which *hedgehog* amino acid sequence of the polypeptide corresponds to a natural proteolytic product of a *hedgehog* protein and (i) binds to a *patched* protein, (ii) regulates differentiation of neuronal cells, (iii) regulates survival of differentiated neuronal cells, (iv) regulates proliferation of chondrocytes, (v) regulates proliferation of testicular germ line cells, or (vi) functionally replaces *Drosophila Hedgehog* in a transgenic *Drosophila* fly, or a combination thereof.
- 15 37. The nucleic acid of claim 35 or 36, wherein the *hedgehog* amino acid sequence is identical to a *hedgehog* protein selected from the group consisting of SEQ ID No:16 and SEQ ID No:17.
- 20 38. An isolated nucleic acid comprising a coding sequence of a human *hedgehog* gene, encoding a bioactive *hedgehog* protein.
- 25 39. An expression vector, capable of replicating in at least one of a prokaryotic cell or a eukaryotic cell, comprising the nucleic acid of claim 35, 36 or 38.

40. A host cell transfected with the expression vector of claim 39 and expressing said recombinant polypeptide.
41. A method of producing a recombinant *hedgehog* polypeptide comprising culturing the cell of claim 40 in a cell culture medium to express a *hedgehog* polypeptide and isolating said *hedgehog* polypeptide from said cell culture.
42. A recombinant transfection system, comprising:
 - (i) a gene construct including the nucleic acid of claim 35, 36 or 38, operably linked to a transcriptional regulatory sequence for causing expression of the *hedgehog* polypeptide in eukaryotic cells, and
 - (ii) a gene delivery composition for delivering said gene construct to a cell and causing the cell to be transfected with said gene construct.
43. The recombinant transfection system of claim 42, wherein the gene delivery composition is selected from a group consisting of a recombinant viral particle, a liposome and a poly-cationic nucleic acid binding agent.
44. A probe/primer comprising a substantially purified oligonucleotide, said oligonucleotide containing a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of SEQ ID No. 7 or 8, or naturally occurring mutants thereof.
45. The probe/primer of claim 44, wherein the probe/primer further comprises a label group attached thereto, wherein said label is capable of being detected.
46. A test kit for detecting cells which contain a *hedgehog* mRNA transcript, comprising the probe/primer of claim 45.
47. A purified preparation of an antisense nucleic acid which specifically hybridizes to and inhibits expression of a gene encoding a human *Ihh* or *Dhh* *hedgehog*

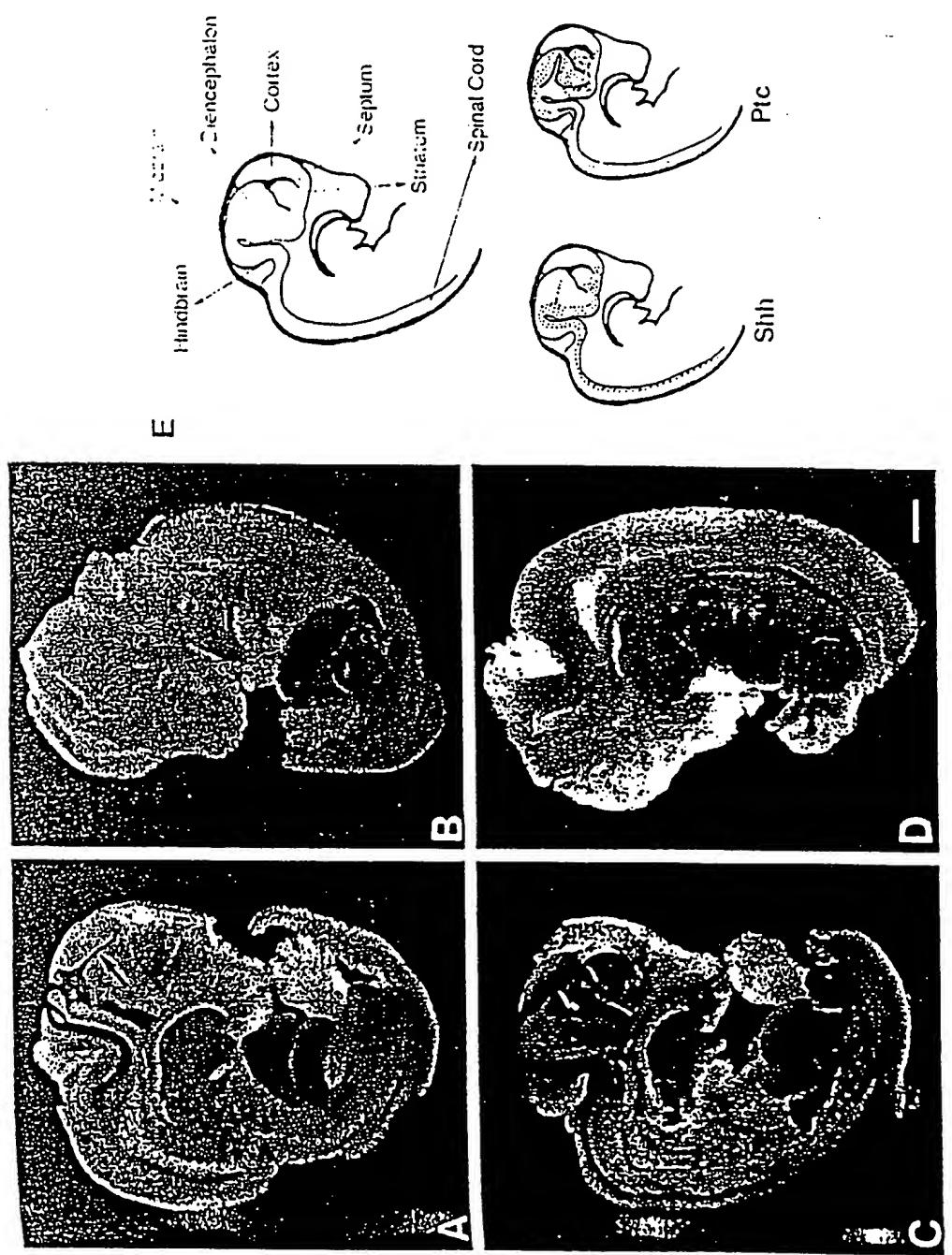
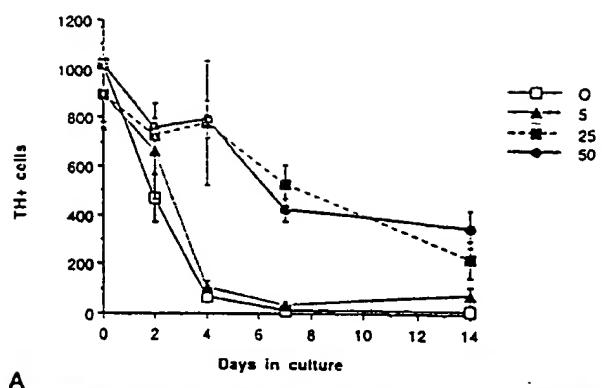


FIG. I



A

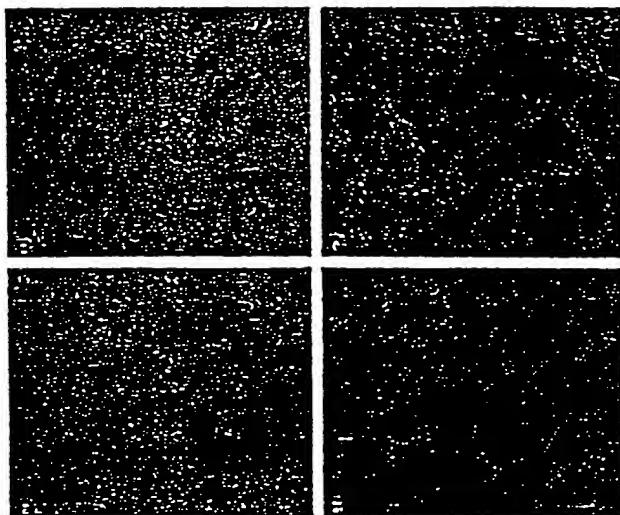
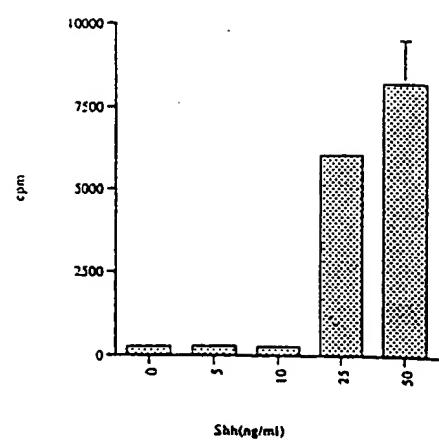


FIG. II



A



FIG. III

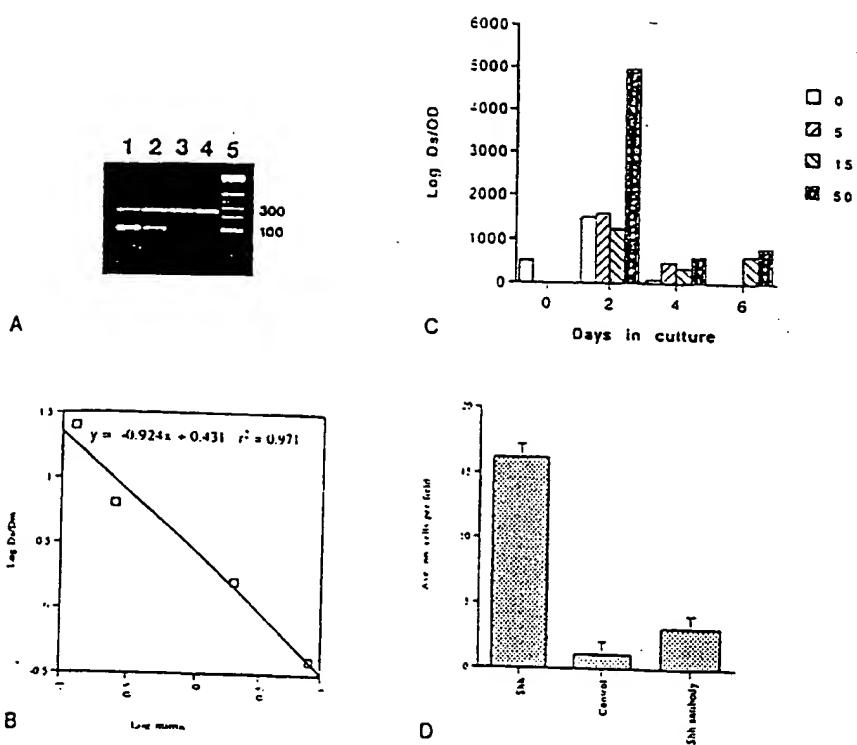
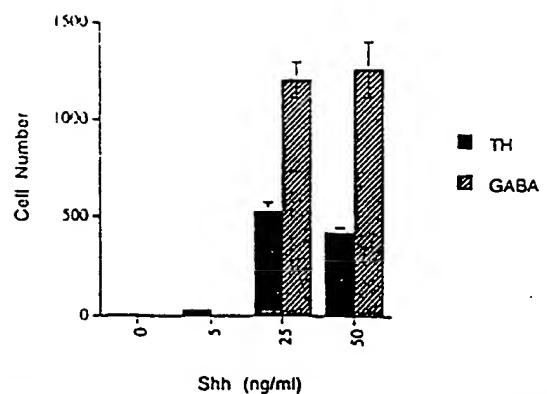


FIG. IV



A



B

FIG. V

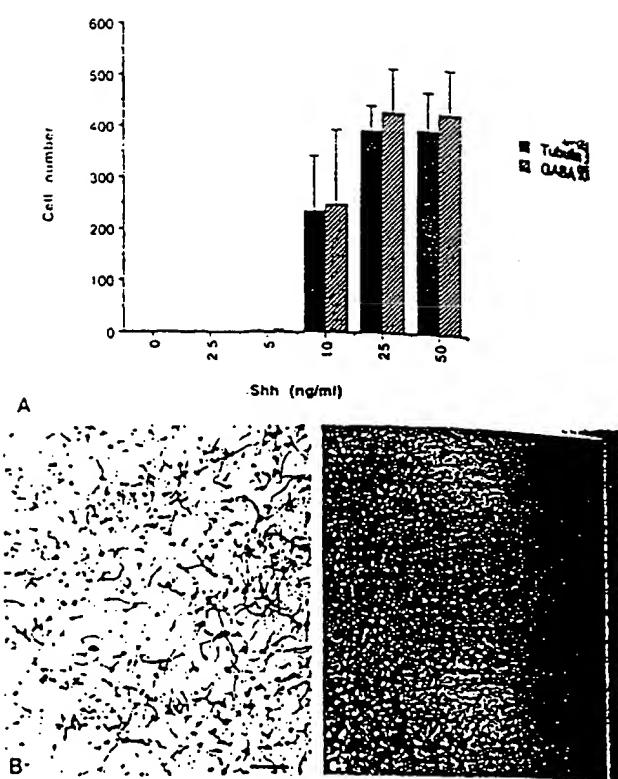


FIG. VI

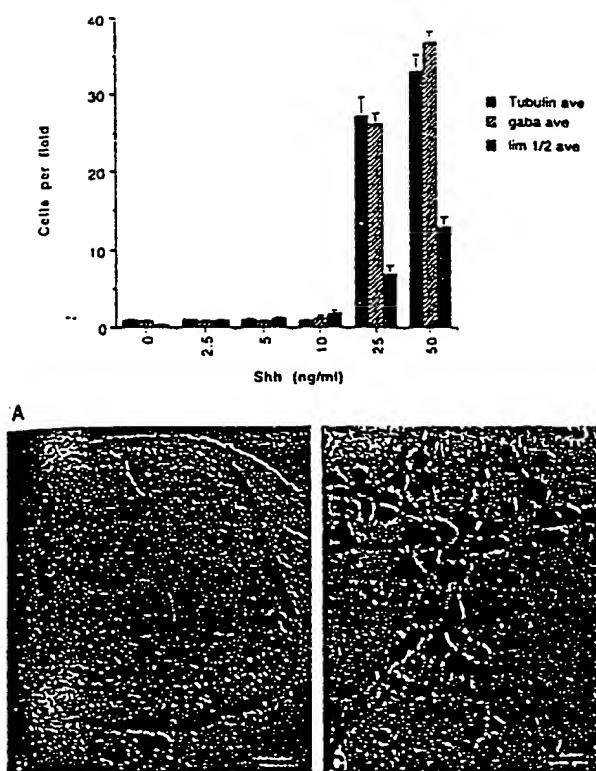


FIG. VII

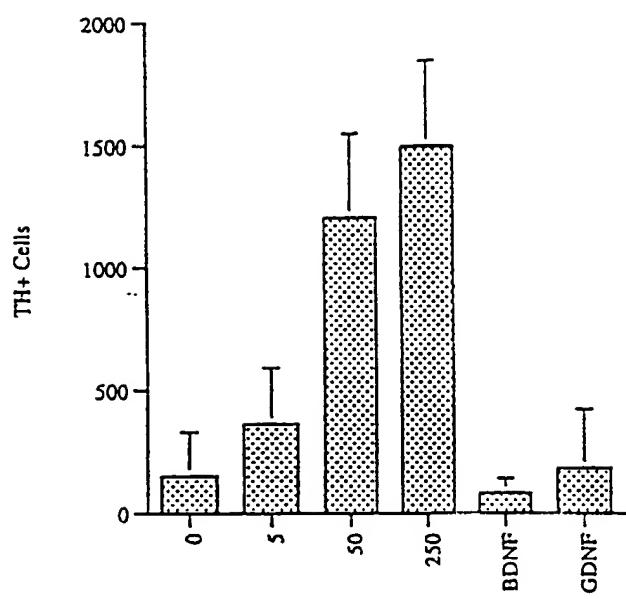


FIG. VIII